Fig. 1A

		_	O1 L			
BTHKURHD flsynbt.fin bssyn	ATGGATAACAA	20 ATCCGAACAT CC	CAATGAATGC	· ★ ★ ₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩	50 * ATTGTTTAAGT CCC.G	60 AACCCTGAA
BTHKURHD flsynbt.fin bssyn	70 GTAGAAGTATT GGGC.(GGGC.(98 AGGTGGAGAA	90 * AGAATAGAA	100 * CTGGTTACAC	110	120
BTHKURHD flsynbt.fin bssyn	130 * TCGCTAACGCAA AGCGCG AGCGCG	140 TTTCTTTTGA	150 AGTGAATTTG	160 TTCCCCCTCCT	170	180
BTHKURHD flsynbt.fin bssyn	190 ** GTTGATATAATA GCCC GCC.	200 rGGGGAATTT	210 TTGGTCCCTC	220 *	230	240
BTHKURHD flsynbt.fin	250 GAACAGTTAATTA .GC.GC. .GC.GC.	260 ACCAAAGAAT	270 *	280	290	300
BTHKURHD G	310 AAGGACTAAGCAA .GCG	320 ATCTTTATCA	330 * AATTTACGCA	340 *	350	360
BTHKURHD CO	370 CTACTAATCCAGC CCCCC	380 ATTAAGAGAA	390 GAGATGCGT	400 *	410	420
BTHKURHD CT	430 TACAACCGCTATT SCCC 490	440	450	460	470	480
BTHKURHD TAT flsynbt.fin	490 ** GTTCAAGCTGCAAGGCC. 550	AATTTACATT	TATCAGTTT1	520 * 'GAGACATICTUTE	530	540
BTHKURHD AGGI	550 ** ********************************	560 CCGCGACTAT	570 * 'CAATAGTCG'	580 *	590	600
					• •	

Fig. 1B

		_				•
BTHKURHD	61 GGC A A C T A T	*			65 <u>0</u>	660
flsynbt.fj bssyn	in	ACAGATCATGO CCC CCC	TGTACGCTGG CG	TACAATACGG	GATTAGAGCG	ŢĠŦĄŦĠĠĠĠĄ
гозуп	••••••		CG	čč.	.cc.g	$C \cdot G \cdot T$
סוועוועוועם	6/(680	690	700	710	720
BTHKURHD flsynbt.fi	CCGGATTCTA nCCAGCC	GAGATTGGAT.	AAGATATAAT	CAATTTAGAA	SAGAATTAACA	* ACTAACTGTA
bssyn	CCAGCC	.CC	žGčč.	GCC.CC.	.CGC.G(.CGC.G(9Çg
	.730	740	750		770	780
BTHKURHD flsynbt.fi	TTAGATATCG	TTTCTCTATTT	* CCGAACTATG	*	*	*
bssyn	č.Gč	.GAGCGC	C C .	.CCCC	CCCC	CCG
	790	800	810		0000	CCG
ВТНКИРНО	* TCCCAATTAA	* ~~~~~~~~~~	*	820	830	840
flsynbt.fir bssyn	AGGC.G. AGGC.G.	CAAGAGAAATT CC.CG	CC	CAGTATTAGA .CGC.G(AAATTTTGAT GCC.	GGTAGTTTT
				.CGC.G(GCC	ččč
BTHKURHD	850	860	870	880	890	900
flsynbt.fin	CGAGGCTCGGC CAGC CAGC	TCAGGGCATA(CC.	GAAGGAAGTAT	TAGGAGTCCA	\CATTTGATGO	ATATACTT
bssýn	CAGC	CČ	Ğčč	cc.ccc	cc	.CCG
DELLEGATION	910	920	930	940	950	960
BTHKURHD flsynbt.fin	AACAGTATAAC	CATCTATACGO	SATGCTCATAG	AGGAGAATAT	TATTGGTCAG	GGCATCAA
bssyn	CC	čč.	.cccc.	CCGC	CAGC.	.CCG
	970	980	990	1000	1010	1020
BTHKURHD	ATAATGGCTTCT	* CCTGTAGGGT	* TTTCGGGGCC	*	*	¥
flsynbt.fin bssyn	CCAGO		.CAGCC(CGC		ATGGAACT .CCC
	1030	1040	1050			
BTHKURHD	*	*	+	1060	1070	1080
flsynbt.fin bssyn	ATGGGAAATGCA	· · A · · T · · G ·	ACGTATTGTT	GCTCAACTAG G.A.G.G.	GTCAGGGCG1	GTATAGA
7	1000	1100		SAGG.	.CA	čč.č
BTHKURHD	1090	1100	1110	1120	1130	1140
flsynbt.fin	ACATTATCGTCCCC.GAGCAGCC.GAGCAG.	ACTTTATATAG CC.GCC.	AAGACCTTTT TC	AATATAGGGA	ТАААТААТСА	ACAACTA
bssÿn		CC.GCC.	ŤČČ	ččč.	.ccc	GGG GGG
·	1150	1160	1170	1180	1190	1200
BTHKURHD flsynbt.fin	TCTGTTCTTGACG	GGACAGAATT	ŢĠĊŢŦĂŢĠĠ <u>Ā</u> ź	ACCTCCTCAA <i>I</i>	* ATTTGCCATC	*
bssyn	ÄĞCGG AGCGG	.CCG(ZCCC.	AG.AGC	CCCAG	CG
				,		••••

Fig. 1C

	12	210	1220	1230	1240	1250	1260
BTHKURHD	TACAGAAA	AAAGCGGA	ACGGTAGATT	CGCTGGATGA GCÇ	AATACCGCCA	CAGAATAACA	ACGTG
flsynbt.fin bssyn	č.č.	.Gč	CGCA	GČČ	SCT	č	• • • • •
	12	270	1280	1290	1300	1310	1320
BTHKURHD	CCACCTAC	GCAAGGA'	TTTAGTCATC	GATTAAGCCA'	IGTTTCAATG	TTTCGTTCAG	GCTTT
flsynbt.fin bssyn	č	AGC	ččč.	.TC.G	CGAGC		č
	13	330	1340	1350	1360	1370	1380
BTHKURHD	AGTAATAG	TAGTGTA	AGTATAATAA	GAGCTCCTAT(GTTCTCTTGG.	ATACATCGTA	GTGCT
flsynbt.fin bssyn	::č::č::	iččg	∴č∴č∴čč	.TA	AGC	Ťčč.	č
	13	390	1400	1410	1420	1430	
BTHKURHD	GAATTTA	TAATATA	ATTCCTTCAT	CACAAATT gcgc	ACACAAATAC	CTTTAACAAA	ATCTA
flsynbt.fin bssyn	GC.	.ccc	cG	GCGC	čgč.	.čč.Ğč	GAGC.
1	440	1450	1460	1470	1480	1490	
втнкияно	CTAATCT	ŗĠĠĊŢĊŢĠ	GAACTTCTGT	CGTTAAAGGA GGGC	CCAGGATTTA	CAGGAGGAGA	TATTC
flsynbt.fin bssyn	.ccc	GAGC.	.CCAGC	GGGC	ččč.	.ččč	čč.
1	500	1510	1520	1530	1540	1550	
BTHKURHD	TTCGAAGA	ACTTCAC	CTGGCCAGAT	TTCAACCTTA CAGCC.G	AGAGTAAATA	TTACTGCACC	ATTAT CC.GA
flsynbt.fin bssyn	.GCC.(C. CAGC.	.č	CAGCC.G	č.čğč.	.ččč	ČČ.GA
1	560	1570	1580	1590	1600	1610	
BTHKURHD	CACAAAGA	ATATCGGG'	TAAGAATTCG	CTACGCTTCT. CAGC	ACCACAAATT	TACAATTCCA	TACAT
flsynbt.fin bssyn	GCGC.	žčč.	.cc.cc	ČAGC	ččč	.ĞĞ	CCA
1	620	1630	1640	1650	1660	1670	٠
BTHKURHD	CAATTGA(CGGAAGAC	СТАТТААТСА	GGGGAATTTT CCC	TCAGCAACTA	TGAGTAGTGG	GAGTA CC.
flsynbt.fin bssyn	GCC	:::cc.c:	.ččč	ččč	ÄĞČČČ.	čč	cc.
1	680	1690	1700	1710	1720	1730	
BTHKURHD	ATTTACA	GTCCGGAA	GCTTTAGGAC	TGTAGGTTTT CGCC	ACTACTCCGT	TTAACTTTTC .CCAG	AAATG CC.
flsynbt.fin bssyn	.čč.g	ÄĞČ.	čč.č	čğčč	ccc.	.CCAG	cc.
. 1	740	1750	1760	1770	1780	1790	
BTHKURHD	CATCAACI	ኮርጥልጥጥጥ ል፡	CGTTAAGTGC	TCATGTCTTC.	AATTCAGGCA	ATGAAGTTTA	TATAG
flsynbt.fin	ርልርር (7 G C	. CC . G C	CCG	CAGC	.CGG	UU.

Fig. 1D

	1	800	1810	1820	1830	1840	1850
BTHKURHD flsynbt.fi bssyn	n	.CC	CGCG	iCCG.	.GC	CGC	GATTTAGAAAGAG CC.GGG. CC.GGG.
	1	860	1870	1880	1890	1900	1910
BTHKURHD flsynbt.fi bssyn	n	.TG	CC	L C.	.CAGCAG	CGC	TTAAAAACAGATG C.GGCC. C.GGCC.
	1	920	1930	1940	1950	1960	1970
BTHKURHD flsynbt.fi bssyn	n	<u>C</u>	TTATCATATT CCCC CCC	GGA	CCAATTTAGT GCC.G	TGAGTGTTTA GCC.G	TCTGATGAATTTT AGCCGC.
	1	980	1990	2000	2010	2020	2030
BTHKURHD flsynbt.fi bssyn	n	GTCTGGA	TGAAAAAAAA CGGG	GAATTGTCCGA	AGAAAGTCAA GG	ACATGCGAAG GCC	CGACTTAGTGATG CGCC.
	2	040	2050	2060	2070	2080	2090
BTHKURHD flsynbt.fi bssyn	n						CTAGACCGTGGCT
	2:	100	2110	2120	2130	2140	2150
BTHKURHD flsynbt.fin bssyn	n	GGAGAGG	AAGTÄCGGAT. CCC	ATTACCATCCA	AAGGÂGGCGA'	rgacgtattca	AAAGÄGAATTACG GC
_	2:	160	2170	2180	2190	2200	2210
BTHKURHD flsynbt.fir bssyn	n						CAAAÂAATAGATG GGCC.
_	22	220	2230	2240	2250	2260	2270
BTHKURHD flsynbt.fir bssyn	n	AGTCGAAA	ATTAÂAAGCC' GC.GG	PATACCCGTTA	ACCAATTAAGA GC.GC.(AGGGTATATCO	GAAGATAGTCAAG .G.C.C.G.
	22	280	2290	2300	2310	2320	2330
BTHKURHD flsynbt.fir bssyn	1	ACTTAGAZ	ATCTATTTA GCC.G	ATTCGCTACAA C	TGCCAAACA(CG	CGAAACAGTAA	ATGTGCCAGGTA
	23	340	2350	2360	2370	2380	2390
BTHKURHD flsynbt.fir bssyn	1	CGGGTTCC .CCAG.	CTTATGGCCGC C.GC	CTTTCAGCCCC .GAGC	AAGTCCAATC	CGGAAAATGTO CGC.	CCCATCATTCCC

Fig. 1E

	24	00	2410	2420	2430	2440	2450
BTHKURHD flsynbt.fir bssyn	า	ATCATTTC	TCCTTGGACA	TTGATGTTGCG	GATGTACAGAC	CTTAAATGAGO C.GC	GACTTAGGTGTAT
		60	2470	2480	2490	2500	2510
BTHKURHD flsynbt.fir bssyn		GGGTGATA	TTCAAGATTA	AGACGCAAGA	ATGGCCATGCA .CC(AAGACTAGGAA CC.CGC	AATCTAGAATTTC CGGC.
	25	20	2530	2540	2550	2560	2570
BTHKURHD flsynbt.fir bssyn	n.	TCGAAGAG	GAAACCATTAG GCC.G.	TAGGAGAAG(.GCG.	CACTAGCTCG	rgrgaaaaga(CGC.C	GCGGAGAAAAAAT CGG.
Dooyii	25	80	2590	2600	2610	2620	2630
BTHKURHD flsynbt.fin bssyn	n	GGAGAGAC C.C	CAAACGTGAAA GCG	AAATTGGAAT(.GCG.	GGGAAACAAA' GC(PATTGTTTATA CCGC	AAAGAGGCAAAAG GCG.
DSSYN	26	540	2650	2660	2670	2680	2690
BTHKURHD flsynbt.finbssyn	n	AATCTGTA	AGATGCTTTAT	TTGTAAACT(CTCAATATGA' GCGC(TAGATTACAA(CC.CC.GG	GCGGATACCAACA
2001	27	00	2710	272 0 .	2730	2740	2750
BTHKURHD flsynbt.firbssyn	n	TCGCGATC	GATTCATGCG(GCAGATAAACO CCG.	GCGTTCATAG GC	CATTCGAGAA CG	GCTTATCTGCCTG CCC.
-	27	760	2770	2780	2790	2800	2810
BTHKURHD flsynbt.fi	n	AGCTGTCT	rgtgattccg(GGTGTCAATG CGC.	CGGCTATTTT .CCC	TGAAGAATTA CGGC.G	GAAGGGCGTATTTGCC.
2001	28	320	2830	2840	2850	2860	2870
BTHKURHD flsynbt.fi bssyn	n	TCACTGCA	ATTCTCCCTA'	TATGATGCGA	GAAATGTCAT .CCG	TAAAAATGGT CGCC 	GATTTTAATAATG CCCC.
200111	28	380	2890	2900	2910	2920	2930
BTHKURHD flsynbt.fi bssyn	n	GCTTATCO C.GAG	CTGCTGGAAC	GTGAAAGGGC GC.	ATGTAGATGT .CGC	AGAAGAACAA GGGG	AACAACCACCGTT CA
	29	940	2950	2960	2970	2980	2990
BTHKURHD flsynbt.fi bssyn	n	CGGTCCT'	rgttgttccg GGGC	GAATGGGAAG GG.	CAGAAGTGTC .CGAG	ACAAGAAGTT CGGG	CGTGTCTGTCCGG CGCC.

Fig. 1F

	30	000	3010	3020	3030	3040	3050
BTHKURHD flsynbt.fir bssyn	า	GTCGTGG(CTATATCCTT(CGTGTCACAGO CGC.	CGTACAAGGA(GGGATATGGA(GAAGGTTGCGTAA GCG.
	30	060	3070	3080	3090	3100	3110
BTHKURHD flsynbt.fir bssyn	1	CCATTCAT	GAGATCGAGA	AACAATACAGA	ACGAACTGAA(GTTTAGCAACT	TGTGTAGAAGAGG CGG
-	31	.20	3130	3140	3150	3160	3170
BTHKURHD flsynbt.fir bssyn	ì	AAGTATATA	CCAAACAACA CC	ACGGTAACGT(GTAATGATTAT	PACTGCGACTC	CAAGAAGAATATG GGC.
•	31	.80	3190	3200	3210	3220	3230
BTHKURHD flsynbt.fir bssyn	1	AGGGTACO	TACACTTCTCCCCCAGC	CGTAATCGAGO .CCC.	GATATGACGGA .CC(AGCCTATGAAA	AGCAATTCTTCTG CAGCAGC.
-	32	240	3250	3260;	3270	3280	3290
BTHKURHD flsynbt.fir bssyn	ì	TACCAGCT	GATTATGCAT	CAGCCTATGA AGCC.	AAGAAAAAGCA .GGGC	TATACAGATO	GGACGAAGAGACA .CCC.C
-	33	800	3310	3320	3330	3340	3350
BTHKURHD flsynbt.fir bssyn	ì	ATCCTTGT	GAATCTAACA	AGAGGATATGO C.CCC.	GGGATTACACA .CC	ACCACTACCAC CCGC.	GCTGGCTATGTGA .CC
•	33	860	3370	3380	3390	3400	3410
BTHKURHD flsynbt.fir bssyn	1	CAAAAGAA .CGG	ATTAGAGTACT GC.G	TCCCAGAAAC	CCGATAAGGTA	ATGGATTGAGA GC	ATCGGAGAAACGG
-	34	20	3430	3440	3450	3460	•
BTHKURHD flsynbt.fir bssyn		AAGGAACA	ATTCATCGTGG	GACAGCGTGGA	AATTACTTCTT .GC.GGC	ATGGAGGAAT GG. TG.	. . G

Fig. 2A

BTHKURHD	10 ATGGATAACAATCO	20 GAACATCAAT	30 * TGAATGCATTO	40 CCTTATAATTO	50 TTTAAGTAAC	60 CCTGAA
bssyn	CC	C	CGC	ccc.	CC.GC	CG
BTHKURHD	70 * GTAGAAGTATTAGG	90 * TGGAGAAG?	90 * ATAGAAACTO	100 * *********************************	110 * *********************************	120 * ייירכייייני
bssyn	GGGC.G	CCGC.0	CCGC		ccc	CAG.C
	130	140	150	160	170	180
BTHKURHD bssyn	TCGCTAACGCAATT AGCGCG	"TCTTTTTGAGT CGCC	GAATTTGTTC	CCGGTGCTGG	CCC.	GGACTA GCG
	190	200	210	220	230	240
BTHKURHD bssyn	GTTGATATAATATG	GGGAATTTTT	TGGTCCCTCT(CCAGC.	CAATGGGACGC .G	ATTTCTTGTA	CAAATT GGC
	25 0	260	270	280	290	300
BTHKURHD bssyn	GAACAGTTAATTAA GC.GC.	CCAAAGAAT <i>A</i>	GAAGAATTCO	CTAGGAACCA	AGCCATTTCT GCAGC	AGATTA C.CC.G
-	310	320	330	340	35 0	360
BTHKURHD bssyn	GAAGGACTAAGCAA	TCTTTATCAP CGC	AATTTACGCAC	GAATCTTTTAG .GAGCCC.	AGAGTGGGAA CG	GCAGAT CC
	370	380	390	400	410	420
BTHKURHD bssyn	CCTACTAATCCAGC	ATTAAGAGAA CC.GC.C.	AGAGATGCGTA	ATTCAATTCAA .CG	TGACATGAAC C	AGTGCC C
	430	440	450	460	470	480
BTHKURHD bssyn	CTTACAACCGCTAT	TCCTCTTTTTCCCC	GCAGTTCAA CCGG.	ATTATCAAGT .CCG	TCCTCTTTTA GCGC.G	TCAGTA GAGCG
	490	50 0	510	52 0	53 <u>0</u>	540
BTHKURHD bssyn	TATGTTCAAGCTGC	AAATTTACAT	TTATCAGTTT C.GAGCGC	TTGAGAGATGT	TTCAGTGTTT CAGCC	GGACAA CG
	55 <u>0</u>	560	57 0	580	590 *	600
BTHKURHD bssyn	AGGTGGGGATTTGA	TGCCGCGACT	ATCAATAGTO	CGTTATAATGA .CCC	TTTAACTAGG CC.GCC.C	CTTATT CGC
	610	62 0	63 <u>0</u>	64 0	65 0	660
BTHKURHD bssyn	GGCAACTATACAGA	TCATGCTGTA	CGCTGGTACA	ATACGGGATT .CCCC.	AGAGCGTGTA GCG	TGGGGA
÷	67 <u>0</u>	680	690	700	710	720
BTHKURHD bssyn	CCGGATTCTAGAGA CCAGCC.C	TTGGATAAGA	TATAATCAAT GCG.	TTAGAAGAGA .CC.CC.C	ATTAACACTA GC.GCG	ACTGTA CG

Fig. 2B

	730	740	750	760	770	780
BTHKURHD bssyn	TTAGATATCGTT C.GC	TCTCTATTTC GAGCGC.	CGAACTATGAT	ragtagaacgt	ATCCAATTC	SAACAGTT .CCG
	790	800	810	820	830	840
BTHKURHD bssyn	TCCCAATTAACA AGGC.GC	AGAGAAATTT <i>I</i> C.CG	ATACAAACCCA CCC	AGTATTAGAAA CGC.GG.	ATTTTGÅTGO .CCC	TAGTTTT CCC
	85 <u>0</u>	860	870	880	890	900
BTHKURHD bssyn	CGAGGCTCGGCT CAGCC	CAGGGCATAGA	AGGAAGTATT GCCC	AGGAGTCCAC	ATTTGATGGA .CC	TATACTT CCG
	910	920	930	940	950	960
BTHKURHD bssyn	AACAGTATAACC	ATCTATACGGA	TGCTCATAGA CCCC.C	GGAGAATATT	ATTGGTCAGG .CAGC	GCATCAA CCG
	970	980	990	1000	1010	1020
BTHKURHD bssyn	ATAATGGCTTCT CCAGC	CCTGTAGGGTT CCC.	TTCGGGGCCA CAGCCC	GAATTCACTT	TTCCGCTATA .CCG	TGGAACT CCC
	1030	1040	1050	1060	1070	1080
BTHKURHD bssyn	ATGGGAAATGCA	GCTCCACAACA ATG	ACGTATTGTT GCCG	GCTCAACTAGO AGG	STCAGGGCGT CA	GTATAGA CC.C
	1090	1100	1110	1120	1130	1140
BTHKURHD bssyn	ACATTATCGTCCA	ACTTTATATAG. CC.GCC.	AAGACCTTTT TCC	AATATAGGGAT	'AAATAATCA CCC	ACAACTA GGG
	1150	1160	1170	1180	1190	1200
BTHKURHD bssyn	TCTGTTCTTGACO	GGACAGAATT' 	IGCTTATGGA CCCC	ACCTCCTCAAA AG.AGC	TTTGCCATCO	CGCTGTA CG
	1210	1220	1230	1240	1250	1260
BTHKURHD bssyn	TACAGAAAAAGCO	GAACGGTAGA' GG	TTCGCTGGAT(CAGCC	GAAATACCGCC GCC	ACAGAATAA(TC	CAACGTG
	1270	1280	1290	1300	1310	1320
BTHKURHD bssyn	CCACCTAGGCAAG	GATTTAGTCAT .CCCC	CGATTAAGCC CTC.G	CATGTTTCAAT CGAGC	GTTTCGTTC <i>I</i>	AGGCTTT TC
	1330	1340	1350	1360	1370	1380
BTHKURHD bssyn	AGTAATAGTAGTG CCCC.	TAAGTATAATA .GCCC	AAGAGCTCCTA C.T.A	ATGTTCTCTTG AGC	GATACATCGT	AGTGCT CC
<i>:</i>	1390	1400	1410	1420	1430	
BTHKURHD bssyn	GAATTTAATAATA GCCC.	TAATTCCTTCA .CC	TCACAAAT GGCG	TACACAAATA CCGC	CCTTTAACAA CC.GC.	AATCTA .GAGC.

Fig. 2C

	1440	1450	1460	1470	1480	1490	
BTHKURHD bssyn	CTAAT .CC	CTTGGCTCTG GAGC.	GAACTTCTGT .CCAGC	CGTTAAAGGA GGGC	CCAGGATTTA CCC.	CAGGAGGAGATA .CCC.	TTC .C.
	1500	1510	1520	1530	1540	1550	
BTHKURHD bssyn	TTCGA .GC	AGAACTTCAC C.CCAGC.	CTGGCCAGAT .C	TTCAACCTTA CAGCC.G	AGAGTAAATA C.CGC.	TTACTGCACCAT	TAT GA
•	1560	1570	1580	1590	1600	1610	
BTHKURHD bssyn	CACAA GCG	AGATATCGGG C.CCC.	TAAGAATTCG .CC.CC	CTACGCTTCT CAGC	ACCACAAATT CCC	TACAATTCCATA .GGC.	.CAT .CA
	1620	1630	1640	1650	1660	1670	
BTHKURHD bssyn	CAATT GCC	GACGGAAGAC	CTATTAATCA .CCC	GGGGAATTTT CCC	TCAGCAACTA AGCCC.	TGAGTAGTGGGA CC.	GTA .C.
	1680	1690	1700	1710	1720	1730	
BTHKURHD bssyn	ATTTA	CAGTCCGGAA AGC.	GCTTTAGGAC	TGTAGGTTTT CGCC	ACTACTCCGT	TTAACTTTTCAA .CCAGC.	ATG .C.
	1740	1750	1760	1770	1780	1790	
BTHKURHD bssyn	GATCA .CAGC	AGTGTATTTA CGC.	CGTTAAGTGC .CC.GC	TCATGTCTTC CCG	AATTCAGGCA CAGC	ATGAAGTTTATA .CGGC.	TAG .C.
	1800	1810	1820	1830	1840	1850	
BTHKURHD bssyn	ATCGA.	ATTGAATTTG' CGC.	TTCCGGCAGA .GCC	AGTAACCTTT GGC	GAGGCAGAAT.	ATGATTTAGAAA .CCC.GG.	.GAG .G.
	1860	1870	1880	1890	1900	1910	
BTHKURHD bssyn	CACAA .TG	AAGGCGGTGA.	ATGAGCTGTT .C	TACTTCTTCC CCAGCAG.	AATCAAATCG CG	GGTTAAAAAACAG .CC.GGC.	ATG .C.
	1920	1930	1940				
BTHKURHD bssyn	TGACG(GATTATCATA'	TTGATCAAGT .CG	ATCC G.AG			

Fig. 3A

cuplT mao	10 ATGGACAACAACC	20 *	30 *	40 *	50 *	60
syn1T.mze bssyn synful.mod	AIGGACAACA	······	·······	······	CCIGAGCAA	·····
symui.mod	70	80	an	100	110	120
syn1T.mze bssyn synful.mod	70 GTGGAGGTGCTGG	80 GCGGCGAGCG	90 CATCGAGÁCCO	100 GGCTACACCC	110 CCATCGACATO	120 CAGCCTG
synful.mod		• • • • • • • • •		• • • • • • • • • •	• • • • • • • • •	
	130	140	150	160	170	180
syn1T.mze bssyn synful.mod	AGCCTGACCCAGT'	TCCTGCTGAG	CGAGTTCGTG(CCCGGCGCCGC	SCTTCGTGCT(GGCCTG
	190	200	210	220	230	240
synlT.mze bssyn synful.mod	GTGGACATCATCT	••			**	GCAGATĈ
• , • •	250	260	270	280	290	300
syn1T.mze bssyn	GAGCAGCTGATCA	ACCAGCGCATO		••		CCGCCTG
synful.mod		• • • • • • • • • • •				
	310	320	330	340	350	360
syn1T.mze	GAGGGCCTGAGCA	ACCTGTACCA(GATCTACGCC(GAGAGCTTCCG	CGAGTGGGAG	GCCGAC
bssyn synful.mod			1	• • • • • • • • •	• • • • • • • •	
	370	380	390	400	410	420
syn1T.mze bssyn synful.mod	CCCACCAACCCCG	CCTGCGCGAG	GGAGATGCGCA	ATCCAGTTCAA	CGACATGAAC	CAGCGCC
	430	440	450	460	470	480
syn1T.mze bssyn synful.mod	CTGACCACCGCCA	rcccctgttc		AACTACĈAGGI	GCCCTGCTG	SAGCGTG
syniai.mod	490	500	510	520	530	540
syn1T.mze bssyn synful.mod	TACGTGCAGGCCGC	* .		*		GGCCAG
syntul.mod	EEO		570	 580	590	600
.· . 1 m	550 *	560 *	*	*	*	*
syn1T.mze bssyn	CGCTGGGGCTTCGA			COCIACAACGA	CCIGACCCGC	·····
synful.mod		· · · · · · · · · · · ·		• • • • • • • • • •	• • • • • • • • •	• • • • • •

Fig. 3B

	610	620	630	640	650	660
syn1T.mze	GGCAACTACACC		GCGCTGGTAC	AACACCGGCC		
bssyn synful.mod	• • • • • • • • • • • •		• • • • • • • • • • • • • • • • • • • •	• • • • • • • • • • •	• • • • • • • • • •	T
	670	680	69 0	700	710	720
synlT.mze	CCCGACAGCCGCC					GACCGTG
bšsyn synful.mod		A . 	G			
•	730	740	750 [%]	760	77 <u>0</u>	780
syn1T.mze	CTGGACATCGTGA	AGCCTGTTCCC	•	AGCCGCACCT.		CACCGTG *
bśsyn synful.mod						
1	790	800	810	820	830	840
syn1T.mze	AGCCAGCTGACCC	GCGAGATCTA		GTGCTGGAGA	* ACTTCGACGG	CAGCTTC
bssyn synful.mod		T.				
•	850	860	870	880	890	900
syn1T.mze	CGCGGCAGCGCCC	* CAGGGCATCGA	* GGGCAGCATC	CGCAGCCCCC	* ACCTGATGGA	CATCCTG
bssyn synful.mod						
•	910	920	930	940	950	960
syn1T.mze	AACAGCATCACCA	••	**		••	CCACCAG
bšsyn synful.mod						
_	970	980	990	1000	1010	1020
syn1T.mze	ATCATGGCCAGCC	^		GAGTTCACCT		CGGCACĈ
bssyn synful.mod		C	• • • • • • • • • •	• • • • • • • • • •		• • • • • • •
	1030	1040	1050	1060	1070	1080
syn1T.mze	ATGGGCAACGCCG	CCCCCCAGCA	GCGCATCGTG	GCCCAGCTGG	GCCAGGGCGT	GTACCGC
bšsyn synful.mod	T.	.AT	• • • • • • • • • •	A	A	
	1090	1100	1110	1120	1130	1140
syn1T.mze			*	×	×	×
9 ,	* ACCCTGAGCAGCA	CCCTGTÂCCG	CCCCCTTC	AACATCGGCAT	CAACAACCA	GCAGCTG
bssyn synful.mod	*	CCCTGTÂCCG	CCGCCCCTTC FAT FAT	AACATCGGCAT	CAACAACCA	GCAGCTG
bssyn	*	1160	CCGCCCCTTC FAT 1170	AACATCGGCAT	TCAACAACCA 1190	GCAGCTG ::::::: 1200
bssyn	ACCCTGAGCAGCA	1160	1170	1180	1190	1200

Fig. 3C

a1Ma	1210	1220	1230	1240	1250	1260
syn1T.mze bssyn synful.mod	TACCGCAAGAGCG	GCACCGTGGA	CAGCCTGGAC	GAGATCCCCC	CCCAGAACAA .T .T	CAACGTG
	1270	1280	1290	1300	1310	1320
syn1T.mze bssyn synful.mod	CCCCCCCGCCAGG ATA ATA	GCTTCAGCCA	CCGCCTGAGC T	CACGTGAGCA		
-	1330	1340	1350	1360	1370	1380
syn1T.mze bssyn synful.mod	AGCAACAGCAGCG	TGAGCATCAT	CCGCGCCCCC TAT			
	1390	1400	1410	1420	1430	1440
syn1T.mze bssyn synful.mod	GAGTTCAACA	TCATCCCCAG	CAGCCAGATC	ACCCAGATCC	CCCTGACCAA	GAGCACC
	1450	1460	1470	1480	1490	1500
syn1T.mze bssyn synful.mod	AACCTGGGCAGCG			CCCGGCTTCA	CCGGCGĞCGA	CATCCTG
	1510	1520	1530	1540	1550	1560
syn1T.mze bssyn synful.mod	CGCCGCACCAGCC				TCACCGCCCC	CCTGAGC
	1570	1580	1590	1600	1610	1620
syn1T.mze bssyn synful.mod	CAGCGCTACCGCG'			ACCACCÂACC'		CACCAGĈ
	1630	1640	1650	1660	1670	1680
synlT.mze bssyn synful.mod	ATCGACGCCCCCC	CCATCAACCA	GGGCAACTTC	AGCGCCACCA'	rgagcagcgg(CAGCAAC
	1690	1700	1710	1720	1730	1740
syn1T.mze bssyn synful.mod	CTGCAGAGCGGCAG					
	1750	1760	1770	1780	1790	1800
synlT.mze bssyn synful.mod	AGCAGCGTGTTCAC					CATCGAC

Fig. 3D

	1810	1820	1830	1840	1850	1860
syn1T.mze	CGCATCGAGTTCGT	GCCCGCCGAG	GTGACCTTC	GAGGCCGAGTA	CGACCTGGAG	CGCGCC A.G. <u>T</u>
bssyn synful.mod						A.GT
	1870	1880	1890	1900	1910	1920
syn1T.mze	CAGAAGGCCĠTGAA	ACGAGCTGTTC	CACCAGCAGC	AACCAGATCG(GCTGAAGACC	:GACGTG
bssyn synful.mod				• • • • • • • •		
-	1930	1940	1950	1960	1970	1980
syn1T.mze	ACCGACTACCACA!	rcgaccaggt(GAGCAACCTG	GTGGAGTGCC'	rgagcgacga(STTCTGC
bssyn synful.mod		T				
_	1990	2000	2010	2020	2030	2040
synlT.mze	CTGGACGAGAAGA	AGGAGCTGAG	CGAGAAGGTG	SAAGCACGCCA	AGCGCCTGAG(CGACGAG
bssyn synful.mod						0100
	2050	2060	2070	2080	2090	2100
syn1T.mze	CGCAACCTGCTGC	AGGACCCCAA	CTTCCGCGG(CATCAACCGCC	AGCTGGACCG	
bssyn synful.mod		• • • • • • • • •			0150	2160
	2110	2120	2130	2140	2150	2160 *
synlT.mze	CGCGGCAGCACCG	ACATCACCAT	CCAGGGCGG	CGACGACGTG1	TCAAGGAGAA	
bssyn synful.mod					2210	2220
	2170	2180	2190	2200 *	2210 * "ACCACAAGAT	2220 * CGACGAG
syn1T.mze bssyn	ACCCTGCTGGGCA	CCTTCGACGA	GTGCTACCC		ACCAGAAGAI	Concorre
synful.mod				2260	2270	2280
	2230	2240	2250	2260	*	
synlT.mze bssyn	AGCAAGCTGAAGC	CCTACACCCC	CTACCAGCT			
synful.mod			0210	2320	2330	2340
	2290	2300	2310	*	*	. *
syn1T.mze bssyn	CTGGAGATCTAC	CTGATCCGC'I'A	ACAACGCCAA			
synful.mod				2380	2390	2400
··	2350	2360	2370	*	*	*
syn1T.mze bssyn	GGCAGCCTGTGG	CCCCTGAGCG(CAICOGCAAG		
synful.mod						

Fig. 3E

		U				
	2410	2420	2430	2440	2450	2460
syn1T.mze	CACTTCAGCCTGG	ACATCGACGTO	GGCTGCACC	GACCTGAACGA	GGACCTGGGC	GTGTGG
bśsyn synful.mod						• • • • •
•	2470	2480	2490	2500	2510	2520
synlT.mze	GTGATCTTCAAGA	TCAAGACCCA(GACGGCCAC	GCCCGCCTGGG	CAACCTGGAG	TTCCTG
bssyn synful.mod						• • • • •
01	2530	2540	2550 -	2560	2570	2580
syn1T.mze	* GAGGAGAAGCCCC	TGGTGGGCGA(CGCGTGAAGCG	CGCCGAGAA	GAAGTGG
bssyn synful.mod						
5 ymrur mou	2590	2600	2610	2620	2630	2640
syn1T.mze	CGCGACAAGCGCG	* AGAAGCTGGA	gTGGGAGACC	AACATCGTGT/	ACAAGGAGGC	
bssyn synful.mod						
Sylliui.mod	2650	2660	2670	2680	2690	2700
1T mgo	AGCGTGGACGCCC	.	*	:GACCGCCTGC	AGGCCGÂCAC	CAACATĈ
syn1T.mze bssyn synful.mod						
Syllul.mod	2710	2720	2730	2740	2750	2760
1m mgo	GCCATGATCCAC	* CCGCCGACAA		AGCATCCGCG.	AGGCCTÂCCT	GCCCGAG
synlT.mze bssyn	GCCATGATCCAC			T		
synful.mod	2770	2780	2790	2800	2810	2820
4	CTGAGCGTGATC		*	* CTTCGAGGAGC		CATCTTC
syn1T.mze bssyn	CTGAGCGTGATC					
synful.mod	2830	2840	2850	2860	2870	2880
	ACCGCCTTCAGC	~~~~ ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	TCCCCAACGT(*	* GCGACTTCA	CAACGGC
syn1T.mze bssyn	ACCGCCTTCAGC					
synful.mod	2000	2900	2910	2920	2930	2940
	2890 CTGAGCTGCTGG	1.	*	*	* CAGAACAACC	
syn1T.mze bssyn	CTGAGCTGCTGG	AHCGIGAAGG				
synful.mod	2050	2960	2970	2980	2990	3000
,·	2950 *	2960 * CCCGAGTGGG	*	GAGCCAGGAG(* GTGCGCGTGT(SCCCCGGC.
syn1T.mze bssyn	GTGCTGGTGGTG					
synful.mod						

Fig. 3F

			•			
	3010 CGCGGCTACATCCT	3020	3030	3040 *	3050 *	3060 *CGTGACC
syn1T.mze	CGCGGCTACATCCT	GCGCGTGACC	GCCTACAAG			
bssyn synful.mod						• • • • •
5 y 11 to 2 v 11 to 4	2070	3080	3090	3100	3110	3120
	3070	3080		••	ACTGCGTGGA(
syn1T.mze	ATCCACGAGATCG	AGAACAACAC	CGACGAGCTG	AAGTTCAGCA		
bśsyn synful.mod			C			
Syntui.mod	2120	21.40	3150	3160	3170	3180
	3130	3140	3150		• • • • • • • • • • • • • • • • • • • •	
syn1T.mze	GTGTACCCCAACA	ACACCGTGAC(CTGCAACGAC	TACACCGCCA	CCCAGGAGGA	
bssyn synful.mod						
syntul.mod		2000	2210	3220	3230	3240
	3190	3200	3210	3220		*
syn1T.mze	GGCACCTACACCA	GCCGCAACCG	CGGCTACGAC	GGCGCCTACG	AGAGCAACAG	CAGCGTG
bssyn						
synful.mod			2070	2200	3290	3300
	3250	3260 ;	3270	3280		
synlT.mze	CCCGCCGACTACG	CCAGCGCCTA	CGAGGAGAA(GCCTACACCC	ACGGCCGCCG	CGACAAC
bssyn synful.mod						
synful.mod			2220	3340	3350	3360
	3310	3320	3330	3340	*.	*
synlT.mze	* CCCTGCGAGAGC	AACCGCGGCTA	CGGCGACTA	CACCCCCTG	CCCGCCGGC'I'A	ACGTGACC
bšsvn						
synful.mod			2200	3400	3410	3420
	3370	3380	3390	3400	*	
syn1T.mze bssyn synful.mod	AAGGAGCTGGAG'	TACTTCCCCGA	AGACCGACAA	GGTGTGGATC	GAGATCGGCG/	AGACCGAG
			2450	3460		
	3430	3440	3450	3460		
syn1T.mze	GGCACCTTCATC	GTGGACAGCG'	TGGAGCTGCT	GCTGATGGAG	GAGTAG	
bssvn						
synful.mod	,,,,,,,,,,		• • • • •			

Fig. 4A

		rig. T			·	
	10	20	30	40	50	60
BTHKURHD	ATGGATAACAATCCG	AACATCAATO	SAATGCATTC(CTTATAATTGT	TTAAGTAACC	CTGAA .A
PMONBT bssyn	ATGGATAACAATCCG CCA CC.	:	Ġċ.	.ccc	Ċ.ĞĊ	.CG
Daayii	70	80	90	100	110	120
חממוזמושם	GTAGAAGTATTAGGI	* 'GGAGAAAGA		GTTACÄCCCCA	ATCGATATTT	CCTTG
BTHKURHD PMONBT	GTAGAAGTATTAGGT TC.T GGGC.GC	0.0 0.00	TC. CGC.	.c	Č.Č	ĠĊ.
bssyn		140	150	160	170	180
	130 TCGCTAACGCAATT	*	* ~~~~mmm~mm~	* CCGGTGCTGG <i>I</i>	X TTTGTGTTA	GGACTA
BTHKURHD PMONBT	TCGCTAACGCAATTT CT.GAG AGCGCGC	GC.CC	GCG.	.Aċċċ	ECTC.C	ĊĊĠ
bssyn	190	200	210	220	230	240
DWINNIDIID	*	* GGGAATTTTT	GGTCCCTCTC	A A TICCCA CCC	ATTTCTTGTA	CAAATT
BTHKURHD PMONBT	GTTGATATAATATGG CCC GCCC	TC	cAAGC.		ċċĠĠ	ĠĊ
bssyn	250	260	270	280	290	300
BTHKURHD	* GAACAGTTAATTAA	* CCAAAGAAT <i>A</i>	GAAGAATTCO	CTAGGAACCA	AGCCATTTCT	AGATTA GG
PMONBT	GAACAGTTAATTAA GGGC GC.GC.	GGC	GG	cc.c	ĞČĀĠĊ	Ċ.ĊĊ.Ğ
bssyn	310	320	330	340	350	360
	GAAGGACTAAGCAA	*	* \ATTTACGCA(GAATCTTTTAG	AGAGTGGGAA	GCAGAT
BTHKURHD PMONBT	GAAGGACTAAGCAA T.G GCG		CTC	GAGCC GAGCCC.	ċ	;čċ
bssyn			390	400	410	420
	370	380	*	* አመመረ አ አመጥር እ 7	* .ጥር ልሮልጥርልል(CAGTGCC
BTHKURHD	CCTACTAATCCAGO	CATTAAGAGA. TC.CC.C	G.A	WIICHWIIOM	Č	C
PMONBT bssyn			G		470	480
	430	440	450 *	460	*	*
BTHKURHD	CTTACAACCGCTA' T.GCA	TTCCTCTTTT	TGCAGTTCAA	AATTATCAAG' CC		GCG
PMONBT bssyn	T.GCA GCC.	.CCG	čcgg	ccg.	.GCGC.	GAGCG
pool	490	500	510	520	530	54U *
BTHKURHD	TATGTTCAAGCTG	CAAATTTACA	TTTATCAGTT	TTGAGAGATG	TTTCAGTGTT AGC	TGGACAA
${ t PMONBT}$	CA. CGGC.	.TC.T	CC.GAGCC	ščč.ċč.	.CAGC	CCG
bssyn	550	560	570	580	590	*
DESTRUCTION	* ACCTGGGGATTTG	ATGCCGCGA(TATCAATAG]	ŢĊĠŦŦĂŢĂĂŢĠ	ATTTAACTAG	GCTTATT
BTHKURHD PMONBT	AGGTGGGGATTTG C.CC.	TA.	.C	žccc.	.cc.gcc.	ĊĞĊ
bssyn	0.0	,5,,,,,,,,				

Fig. 4B

		1 16. 12	_			
	610	620	630 *	640	65 0	660
BTHKURHD	GGCAACTAŢĀCAGA	TCATGCTGTA	CGCTGGTACA	ATACGGGATTA	GAGCGTGTA	TGGGGA
PMONBT	GGCAACTATACAGA ACC CC	$\mathbb{C} \cdot \cdot \mathbb{C} \cdot \cdot \cdot \mathbb{T}$	T	.CTC6	i i i i i i i i i i i i i i i i i i i	T
bssyn		UUUG				
•	670	680	690	700 *	710	720
ВТНКURHD	* CCGGATTCTAGAGA	TTGGATAAGA'	ГАТААТСААТ	TTAGAAGAGAF	ATTAACACTA	ACTGTA
PMONBT	CCGGATTCTAGAGA TCAĠĊĊ.Ċ	$\vdots \cdots \overset{\mathrm{T}}{\vdash} \cdots \overset{\mathrm{c}}{\vdash}$			c.GCG	ĈĠ
bssyn	CCAGCC.C				770	780
	730	740	750 '	760	*	*
BTHKURHD	* TTAGATATCGTTTC	TCTATTTCCG	AACTATGATA	AGTAGAACGTA'	CCAATTCGA	ACAGTT
PMONBT	TTAGATATCGTTTC GCTG C.GCGAG			ČČĊ.ĊČ	ćċč	CG
bssyn			810	820	830	840
	790	800	·	*	*	* ************************************
BTHKURHD	TCCCAATTAACAAC	SAGAAATTTAT	ACAAACCCA(GTATTAGAAAA'	PTTGATGG	AGITII
PMONBT	TCCCAATTAACAAG AGC.TC. AGGC.GCC.			GC .GG	ččč(cc
bssyn	AGGC.GCC.			880	890	900
	850	860	87 <u>0</u>	*	*	*
BTHKURHD	CGAGGCTCGGCTC	AGGGCATAGAA	GGAAGTATT	AGGAGTCCACA	TTTGATGGA'	
PMONBT	CGAGGCTCGGCTCA TTTC. CAGCC.	ATC	C^{TCC}		čċ	ččg
bssyn	CAGCC.				050	960
	910	920	930	940	950	*
BTHKURHD	* AACAGTATAACCA'	rctatacgga1	TGCTCATAGA	GGAGAATATTA	TTGGTCAGG	GCATCAA A CG
PMONBT	AACAGTATAACCA' CT. CC	g.gc	۲۰۰۶، ۲۰۰۶، ۲	C. G. C.	Č. AGČ.	ĊčĞ
bssyn	CC					1020
	970	980	990	1000	1010	*
DWINIDID	ATAATGGCTTCTC	CTGTAGGGTT'	TTCGGGGCCA	GAATTCACTTI	TCCGCTATA	TGGAACT
BTHKURHD PMONBT	ATAATGGCTTCTCCCAGC.	.ATA	CAGCC	G.T.C.	ĊĊĞ	ċ∷ċ∷ċ
bssyn	CCAGC.	.0	CAGCCC	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		1080
	1030	1040	1050	1060	1070	*
	ATGGGAAATGCAG	CTCCACAACA	ACGTATTGTT	GCTCAACTAG(STCAGGGCGT	GTATAGA
BTHKURHD PMONBT	AIGGGAAAIGCAC		cc	GOTOMOTHO.	Ċ	cc.c
bssyn	ccc.	.ATG	6			1140
-	1090	1100	1110	1120	1130	1140
	* ACATTATCGTCCA	▗Ċ₼₼₼₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	AAGACCTTTT	raatataggga'	raaataatc <i>i</i>	ACAACTA
BTHKURHD PMONBT	ACATTATCGTCCA	.CGC		\mathbb{Z} \mathbb{Z} .	.cgç	G.G.G
bssyn	CGT CC.GAGCAG	.cc.gcc.	TC			
- .	1150	1160	1170	1180	1190	1200
·	*	⋆ ͻϲϲልሮልርልሽͲͲ	maamma mcc	AACCTCCTCAA	ATTTGCCAT(CCGCTGTA
BTHKURHD PMONBT	TCTGTTCTTGACC	AG	<u>C</u> <u>C</u>	\dots T T	.C	T. C. G
bssyn	AGCGG	ccg	CCC	CAG.AGC.		.,

Fig. 4C

			1 15.				
	1	210	1220	1230	1240	1250	1260
BTHKURHD	TACAGA	AAAGCGGA	ACGGTAGATT	CGCTGGATC	GAAATACCGC	CACAGAATAA	CAACGTG
PMONBT							
bssyn	C.C.	.GC					1320
	•	1270	1280	1290	1300	1310	*
BTHKURHD	CCACCT	AGGCAAGGA	TTTAGTCAT	CGATTAÁGC	CATGTTTCAA	TGTTTCGTTC	AGGCTTT
PMONBT	C		ctccc	A.GG	CGAGC.	ČĊĀĊ	TČ
bssyn	(C.AGC				1270	1380
		1330	1340	1350	1360	1370	*
BTHKURHD	AGTAAT.	AGTAGTGT <i>A</i>	AGTATAATA	AGAGCTCCT	ATGTTCTCTT	GGATACATC	FAGTGCT
PMONBT	çç	TCC9	3220	Ċ.Ť.Á	Ä. ÄGC.	ŤĊ.	.cc
bssyn					1420	1430	
		1390	1400	1410	*	*	አ አ አ ጥ ር ጥ
BTHKURHD	GAATTT	AATAATAT	ATTCCTTCA		TTACACAAAT .CC	I A 17	
PMONBT	gç	cc]C	Ġ. GC. Ġ.	.ccg.	.ccc.g	CGAGC.
bssyn				1470	1480	1490	
	1440	1450	1460			* CACACCACT	АСАТАТТС
BTHKURHD	CTAATO	TTGGCTCT	GGAACTTCT	GTCGTTAAAC G	GACCAGGAT'	.C	T
PMONBT	.cc.	ĠĀĠĊ		.GGG	∷ċ∷ċ∷č:	.ccc	CCC.
bssyn		1510	1520	1530	1540	1550	
	1500	*		*	* TTAAGAGTAA	ATATTACTGC	ACCATTAT
BTHKURHD	TTÇGA	AGAACTTCA T	CCTGGCCAG	AGC	C.CT.	.çç	C.C.T.
PMONBT bssyn	A .GC	Ċ.ĊĊĂĠĊ		CAGC	c.gc.cg.	.000.	CCGA
DSSYII		1570	1580	1590	1600)
	1560	*	*	* ጥርርጥአርርርጥ	TCTACCACAA	ATTTACAATT	CCATACAT
BTHKURHD	CACAA	AGATATCGO T	GTAAGAATT	TA	AGCC.	.cg	C C
PMONBT bssyn	ĠĊ⋰Ġ	c.ccc	ccc.cc				
2001	1620	1630	1640	1650	1669	16/0) *
	*	*	የሚፈመው መመን እጥ	* TAGGGGAAT	TTTTCAGCAA	CTATGAGTA	GŢGGĢAGŢA
BTHKURHD	CAA'I'I'	GACGGAAGA	3C	ŢĈ	cc	TCA.	.ccc.
PMONBT bssyn	ĠĊŨĊ	cc.	cccc	:CC	TTTTTCAGCAP	173	0
	1600	1690	1700	1710) 1729) 1/3	V *
	*	*	* አአርሮሞሞጥΔር(· ACTGTAGGT	TTTTACTACT(CCGTTTAACT	TTTCAAATG
BTHKURHD	A'T'T'F	CAGTCCGG.	CC		TTTACIACI CCC	T C C . C	CÁGC. C
PMONBT bssyn	.čċ.d	AG	ccc.(366		4.50	
•	1740	1750	1760	177(ı ·	*
	* *	* ለአርጥርጥአጥጥ	* 'ግልርርሞሞልልር'	rGCTCATGT(* CTTCAATTCA GT	GGCAATGAAG	TTTATATAG
BTHKURHD PMONBT	GATCE	CŢ	ĊCC.T	Ž	GCAGC	ċĠ.	.Gcc.
bssyn	.CAG	CCG	CCC.G				

Fig. 4D

BTHKURHD PMONBT bssyn	1800 ATCGA .CT	1810 ATTGAATTTG	1820 GTTCCGGCAGA .GTC .GCC	1830 AAGTAACCTTT TC .GGC	GAGGCAGAATA TG	 CGACCTGGAGAGGG
BTHKURHD PMONBT bssyn	CTCAC	GAAGGCCGTGA	AACGAGCTGT	rcaccagcago	CAACCAGATCGG	 CCTGAAGACCGACG
BTHKURHD PMONBT bssvn	 TGAC	CGACTACCAC	ATCGATCAGG	T C TGTAG		.*

Fig. 5A

		.				
	10	20	30	40	50 *	60 *
PMONBT	ATGGACAACAACCC	AAACATCAAC	GAATGCATTC GC.	CATACAACTGO .C	TTGAGTAACC CC	CG
bssyn	70	80	90	100	110	120
PMONBT	* GTTGAAGTACTTGGGGG	TGGAGÂACGC	ATTGAAACCG	GTTACACTCC	CATCGACATC'	rccttg Ag.C
bssyn	130	140	150	160	170	180
PMONBT	* TCCTTGACACAGTT	TCTGCTCAGC	GAGTTCGTGC	CAGGTGCTGG	GTTCGTTCTC	GGACTA CG
bssyn	AG.CC 190	200	210	220	230	240
PMONBT	GTTGACATCATCT	* GGGTATCTTI	GGTCCATCTC	CAATGGGATGC	ATTCCTGGTG	
bssyn	G	CC 260	270	280	290	300
DMONDE	250 GAGCAGTTGATCA		٠.	* GCCAGGAACCA	GGCCATCTCT	AGGTTG C.CC
PMONBT bssyn	C			C.C 340	350	360
	310 GAAGGATTGAGCA	320 *	330 * * apcpapgca	* GAGAGCTTCAG	* SAGAGTGGGAA	GCCGAT
PMONBT bssyn	GCC	.CG				420
	370	380	390 *	400 ATTCAATTCA	410 * \CGACATGAA(*
PMONBT bssyn		CTCTCCGCGA .CG	GGAAATGCGT. GC	CG		• • • •
2001	430	440	450 *	460	470 *	480 * cmcccmc
PMONBT	TTGACCACAGCTA	TCCCATTGTT	CGCAGTCCAGCG	AACTACCAAG'	.GCGC.	. AO
bssyn	490	500	510	520 *	530	540
PMONBT	TACGTTCAAGCAG	CTAATCTTCA CCG	CCTCAGCGTG	CTTCGAGACG	TTAGCGTGTT .C	TGGGCAA CCG
bssyn	550	560	570	580	59 0	600
PMONBT	AGGTGGGGATTCC C.CC	SATGCTGCAAC	CATCAATAG(CCGTTACAACG	ACCTTACTAGGCC.	GCTGATT CC
bssyn	C.CC	620	630	640	650	660
PMONBT	GGAAACTACACC C	GACCACGCTG	r <u>T</u> CGTTGGTA	CAACACŢĠGCŢ	TGGAGCGTGT	CTGGGGT
bssyn		680	.GC	700	710	720
	670 * CCTGATTCTAGA CCAGCC.C	GATTGGATTA	GATACAACCA		AATTGACCCI	CACAGTT
PMONBT bssyn	CCAGCC.C	cc.	.G		, , , , , , , , , , , , , , , , , , , ,	,

Fig. 5B

		7 -0, -			.*	
	730	740	750 *	760	770	780
PMONBT bssyn	TTGGACATTGTGTCT	CTCTTCCCC	GAACTATGACT	CCAGAACCTA G.C.C	CCCTATCCGT CC	ACAGTG C
DSSYII	790	800	810	820	830	840
PMONBT bssyn	TCCCAACTTACCAGA AGGGC.	GAAATCTAT	TACTAACCCAC CCC.	TTCTTGAGAA .GG	CTTCGACGGT	AGCTTC
D00 1.1	850	860	870	880	890	900
PMONBT bssyn	CGTGGTTCTGCCCA CCAGC	AGGTATCGA GC	AGGCTCCATCA GAG(AGGAGCCCACA C.CC	CTTGATGGAC .C	CATCTTG
booy	910	920	930	940	950	960
PMONBT bssyn	AACAGCATAACTAT	CTACAGCGA'	TGCTCACAGA(CCC.C	GGAGAGTATT <i>I</i> CC.	ACTGGTCTGGA	
2001	970	980	990	1000	1010	1020
PMONBT bssyn	ATCATGGCCTCTCC	AGTTGGATT CCC	CAGCGGGCCC(GAGTTTACCT.		
2001	1030	1040	1050	1060	1070	1080
PMONBT bssyn	ATGGGAAACGCCGC	TCCACAACA ATG	ACGTATCGTT GCG	GCTCAACTAG AGG.	.CA	
2001	1090	1100	1110	1120	1130	1140
PMONBT bssyn	ACCTTGTCTTCCAC CAGCAG	CTTGTACAC	AAGACCCTTC TCT	AATATCGGTA CC.	TCAACAACCA	
2001	1150	1160	1170	1180	1190	1200 * *
PMONBT bssyn	TCCGTTCTTGACGC AGGG	SAACAGAGTT .CC	CGCCTATGGA	ACCTCTTCTA AGCAGC.	CCAG	
2007	1210	1220	1230	1240	1250	1260
PMONBT bssyn	TACAGAAAGAGCG(GAACCGTTGA .CG.	ATTCCTTGGAC .CAG.C	GAAATCCCAC GC.		
2007	1270	1280	1290	1300 *	1310 *	1320 *
PMONBT bssyn	CCACCCAGGCAAG TC.AG.	GATTCTCCC. .CAG	ACAGGTTGAGG	AG.		
	1330	1340	1350	1360 *	1370 * "CCNTTCNTC	1380 * TAGTGCT
PMONBT bssyn	AGCAACAGTTCCG	TGAGCATCA	TCAGAGCTCC	• • • •		
	1390	1400	1410	1420 *	1430 * **********************************	1440 * AGTCTACT
PMONBT bssyn	GAGTTCAACAATA	TCATTCCTTCCA	CCTCTCAAAT G.AGCG	CACCCAAATC	CC	ÄĞÇÇ

Fig. 5C

	1450	1460	1470	1480	1490	1500
PMONBT	AACCTTGGATCTGCGCAGC.	GAACTTCTGT(.CCAGC(CGTGAAAGGAC GGC	CAGGCTTCAC	CAGGAGGTGAT .CCC	ATTCTT CG
bssyn	1510	1520	1530 '	1540	1550	1200
PMONBT bssyn	AGAAGAACTTCTC C.CC.CCAGC.	CTGGCCAGAT'	TAGCACCCTC CG	AGAGTTAACA' C.CG	CACTGUACUA CC(
2007	1570	1580	1590	1600	1610	1620 *
PMONBT bssyn	CAAAGATATCGTG GC.CC.	TCAGGATTCG C.CC	TTACGCATCT CCAGC	ACCACTAACT CC	TGCAATTCCAC	
pssyn	1630	1640	1650	1660	1670	1680
PMONBT bssyn	ATCGACGGAAGGC	CTATCAATCA .CC	GGGTAACTTC C	TCCGCAACCA AGC	TGTCAAGCGG AGC	
pssyn	1690	1700	1710	1720	1730	1740
PMONBT	TTGCAATCCGGCA	AGCTTCAGAAC	CCGTCGGTTTC GC	CACTACTCCTT CCC.	TCAACTTCTC AG	
bssyn	1750	1760	1770	1780	1790	1800
PMONBT bssyn	TCAAGCGTTTTCA AGCG	ACCCTTAGCG	CTCATGTGTT(.CC	CAATTCTGGC1 CAGC	AATGAAGTGTA CG	C
p001	1810	1820	1830	1840		
PMONBT bssyn	CGTATTGAGTTT CCC	GTGCCTGCCG	AAGTTACCTT(.GG	CGAGGCTGAG' C	CGACCTGGA	AGAGGGCT
PMONBT bssyn	CAGAAGGCCGTG	AACGAGCTGT	TCACCAGCAG	CAACCAGATC	GGCCTGAAGA	CCGACGTG
PMONBT bssyn	ACCGACTACCAC	ATCGATCAGG	C GTGTAG		·	

Fig. 6A

64	ATGGACCTGC TGCCCGACGC CCGCATCGAG GACAGCCTGT GCATCGCCGA GGGCAACAAC MetAspLeu LeuProAsp AlaArgIleGlu AspSerLeu CysIleAla GluGlyAsnAsn	
124	ATCGACCCCT TCGTGAGCGC CAGCACCGTG CAGACCGGCA TCAACATCGC CGGCCGCATC	
184	CTGGGCGTGC TGGGCGTGCC CTTCGCCGGC CAGCTGGCCA GCTTCTACAG CTTCCTGGTG	-
244	GGCGAGCTGT GGCCCCGCGG CCGCGACCAG TGGGAGATCT TCCTGGAGCA CGTGGAGCACACACACACACACACACACACACACACACAC	1
304	CTGATCAACC AGCAGATCAC CGAGAACGCC CGCAACACCG CCCTGGCCCG CCTGCAGGGC LoulleAsn GlnGlnIle ThrGluAsnAla ArgAsnThr AlaLeuAla ArgLeuGlnGl	ĺ
364	CTGGGCGACA GCTTCCGCGC CTACCAGCAG AGCCTGGAGG ACTGGCTGGA GAACCGCGAG LouglyAsp SerPheArg AlaTyrGlnGln SerLeuGlu AspTrpLeu GluAsnArgAs	O
424	GACGCCCGCA CCCGCAGCGT GCTGTACACC CAGTACATCG CCCTGGAGCT GGACTTCCT	u
484	AACGCCATGC CCCTGTTCGC CATCCGCAAC CAGGAGGTGC CCCTGCTGAT GGTGTACGC	a
544	CAGGCCGCCA ACCTGCACCT GCTGCTGCTG CGCGACGCCA GCCTGTTCGG CAGCGAGII	e
604	GGCCTGACCA GCCAGGAGAT CCAGCGCTAC TACGAGCGCC AGGTGGAGCG CACCCGCGA GlulauThr SarGlaglu lleGlaArgTyr TyrGluArg GlaValGlu ArgThrArgAs	p
664	TACAGCGACT ACTGCGTGGA GTGGTACAAC ACCGGCCTGA ACAGCCTGCG CGGCACCAA TURSORASD TYPCYSVal GluTrpTyrAsn ThrGlyLeu AsnSerLeu ArgGlyThrAs	n
724	GCCGCCAGCT GGGTGCGCTA CAACCAGTTC CGCCGCGACC TGACCCTGGG CGTGCTGGA	p
784	CTGGTGGCCC TGTTCCCCAG CTACGACACC CGCACCTACC CCATCAACAC CAGCGCCCA	n
844	CTGACCCGCG AGGTGTACAC CGACGCCATC GGCGCCACCG GCGTGAACAT GGCCAGCAL	et
904	AACTGGTACA ACAACACGC CCCCAGCTTC AGCGCCATCG AGGCCGCCGC CATCCGCAC	er
964	CCCCACCTGC TGGACTTCCT GGAGCAGCTG ACCATCTTCA GCGCCAGCAG CCGCTGGAG	er
1024	CTCCCCCCC CACACCATCC AGAGCCGCCC CALCEGGCG	ين Ly

Fig. 6B

1084	GGCCTGAACA CCAGCACCCA CGGCGCCACC AACACGlyLeuAsn ThrSerThr HisGlyAlaThr AsnTh	CCAGCA TCAACCCCGT GACCCTGCGC hrSer IleAsnPro ValThrLeuArg
1144	TTCGCCAGCC GCGACGTGTA CCGCACCGAG AGCTA PheAlaSer ArgAspVal TyrArgThrGlu SerT	ACGCCG GCGTGCTGCT GTGGGGCATC yrAla GlyValLeu LeuTrpGlyIle
1204	TACCTGGAGC CCATCCACGG CGTGCCCACC GTGCC	GCTTCA ACTTCACCAA CCCCCAGAAC rgPhe AsnPheThr AsnProGlnAsn
1264	ATCAGCGACC GCGGCACCGC CAACTACAGC CAGC	CCTACG AGAGCCCCGG CCTGCAGCTG roTyr GluSerPro GlyLeuGlnLeu
1324	AAGGACAGCG AGACCGAGCT GCCCCCCGAG ACCA	CCGAGC GCCCCAACTA CGAGAGCTAC hrGlu ArgProAsn TyrGluSerTyr
1384	AGCCACCGCC TGAGCCACAT CGGCATCATC CTGC	AGAGCC GCGTGAACGT GCCCGTGTAC lnSer ArgValAsn ValProValTyr
1444	AGCTGGACCC ACCGCAGCGC CGACCGCACC AACA	CCATCG GCCCCAACCG CATCACCCAG hrIle GlyProAsn ArgIleThrGln
1504	ATCCCCATGG TGAAGGCCAG CGAGCTGCCC CAGG	GCACCA CCGTGGTGCG CGGCCCCGGC lyThr ThrValVal ArgGlyProGly
1564	TTCACCGGCG GCGACATCCT GCGCCGCACC AACA	ACCGGCG GCTTCGGCCC CATCCGCGIG ThrGly GlyPheGly ProIleArgVal
1624	ACCGTGAACG GCCCCCTGAC CCAGCGCTAC CGCA	ATCGGCT TCCGCTACGC CAGCACCGTG [leGly PheArgTyr AlaSerThrVal
1684	GACTTCGACT TCTTCGTGAG CCGCGGCGGC ACCA	ACCGTGA ACAACTTCCG CTTCCTGCGC ThrVal AsnAsnPhe ArgPheLeuArg
1744	ACCATGAACA GCGGCGACGA GCTGAAGTAC GGCA	AACTTCG TGCGCCGCGC CTTCACCACC AsnPhe ValArgArg AlaPheThrThr
1804	4 CCCTTCACCT TCACCCAGAT CCAGGACATC ATC	CGCACCA GCATCCAGGG CCTGAGCGGC ArgThr SerIleGln GlyLeuSerGly
1864	4 AACGGCGAGG TGTACATCGA CAAGATCGAG ATC	ATCCCCG TGACCGCCAC CITCGAGGCC IlePro ValThrAla ThrPheGluAla
1924	4 GAGTACGACC TGGAGCGCGC CCAGGAGGCC GTG	AACGCCC TGTTCACCAA CACCAACCCC AsnAla LeuPheThr AsnThrAsnPro
1984	4 CGCCGCCTGA AGACCGACGT GACCGACTAC CAC	ATCGACC AGGTGAGCAA CCTGGIGGCC IleAsp GlnValSer AsnLeuValAla
2044	THE TARK CHARGE COMMON AND	CGCGAGC TGCTGGAGAA GGTGAAGTAC ArgGlu LeuLeuGlu LysValLysTyr
. "	•	

Fig. 6C

2104	GCCAAGCGCC TGAGCGACGA GCGCAACCTG CTGCAGGACC CCAACTTCAC CAGCATCAAC AlaLysArg LeuSerAsp GluArgAsnLeu LeuGlnAsp ProAsnPhe ThrSerIleAsn
2164	AAGCAGCCCG ACTTCATCAG CACCAACGAG CAGAGCAACT TCACCAGCAT CCACGAGCAG LysGlnPro AspPheIle SerThrAsnGlu GlnSerAsn PheThrSer IleHisGluGln
2224	AGCGAGCACG GCTGGTGGGG CAGCGAGAAC ATCACCATCC AGGAGGGCAA CGACGTGTTC SerGluHis GlvTrpTrp GlySerGluAsn IleThrIle GlnGluGly AsnAspValPhe
2284	AAGGAGAACT ACGTGACCCT GCCCGGCACC TTCAACGAGT GCTACCCCAC CTACCTGTAC LysGluAsn TyrValThr LeuProGlyThr PheAsnGlu CysTyrPro ThrTyrLeuTyr
2344	CAGAAGATCG GCGAGAGCGA GCTGAAGGCC TACACCCGCT ACCAGCTGCG CGGCTACATC
2404	GAGGACAGCC AGGACCTGGA GATCTACCTG ATCCGCTACA ACGCCAAGCA CGAGACCCTG GAGGACAGCC GIuAspSer GlnAspLeu GluIleTyrLeu IleArgTyr AsnAlaLys HisGluThrLeu GluAspSer GlnAspLeu GluIleTyrLeu IleArgTyr AsnAlaLys HisGluThrLeu
2464	GACGTGCCCG GCACCGAGAG CCTGTGGCCC CTGAGCGTGG AGAGCCCCAT CGGCCGCTGC
2524	GGCGAGCCCA ACCGCTGCGC CCCCCACTTC GAGTGGAACC CCGACCTGGA CTGCAGCTGC Cluclupro AsnArgCvs AlaProHisPhe GluTrpAsn ProAspLeu AspCysSerCys
2584	CGCGACGGCG AGAAGTGCGC CCACCACAGC CACCACTTCA GCCTGGACAT CGACGTGGGC ArgAspGly GluLysCys AlaHisHisSer HisHisPhe SerLeuAsp IleAspValGly
2644	TGCACCGACC TGCACGAGAA CCTGGGCGTG TGGGTGGTGT TCAAGATCAA GACCCAGGAG CysThrAsp LeuHisGlu AsnLeuGlyVal TrpValVal PheLysIle LysThrGlnGlu
2704	GGCCACGCCC GCCTGGGCAA CCTGGAGTTC ATCGAGGAGA AGCCCCTGCT GGGCGAGGCC GlyHisAla ArgLeuGly AsnLeuGluPhe IleGluGlu LysProLeu LeuGlyGluAla
2764	CTGAGCCGCG TGAAGCGCGC CGAGAAGAAG TGGCGCGACA AGCGCGAGAA GCTGCAGCTG LeuSerArg VallysArg AlaGluLysLys TrpArgAsp LysArgGlu LysLeuGlnLeu
2824	GAGACCAAGC GCGTGTACAC CGAGGCCAAG GAGGCCGTGG ACGCCCTGTT CGTGGACAGC
2884	CAGTACGACC GCCTGCAGGC CGACACCAAC ATCGGCATGA TCCACGCCGC CGACAAGCTG CAGTACGACCAAC ATCGGCATGA TCCACGCCGC CGACAAGCTG CAGTACGACACAAC ATCGGCATGA TCCACGCCGC CGACAAGCTG CAGTACGACAACAACAACAACAACAACAACAACAACAACAACAA
2944	GTGCACCGCA TCCGCGAGGC CTACCTGAGC GAGCTGCCCG TGATCCCCGG CGTGAACGCC
3004	TCACCCCA CATC ATCACCGCCA TCAGCCTGTA CGACGCCGC

Fig. 6D

3064	AACGTGGTGA AGAACGGCGA CTTCAACAAC GGCCTGACCT GCTGGAACGT GAAGGGCCAC ASNValVal LysAsnGly AspPheAsnAsn GlyLeuThr CysTrpAsn ValLysGlyHis
3124	GTGGACGTGC AGCAGAGCCA CCACCGCAGC GACCTGGTGA TCCCCGAGTG GGAGGCCAACGAGTG GAACGAGTG GGAGGCCAACGAGTG GAACGAGTG GAACGAGAGTG GAACGAGTG GAACGAGTG GAACGAGAGTG GAACGAGTG GAA
3184	GTGAGCCAGG CCGTGCGCGT GTGCCCCGGC TGCGGCTACA TCCTGCGCGT GACCOCATAGA TCCTGCGCGT GACCATAGA TCCTGCGCGT GACCOCATAGA TCCTGCGCGT GACCOCATAGA TCCTGCGCGT GACCOCATAGA TCCTGCGCGT GACCATAGA TCCTGCGCGT GACCATAGA TCCTGCGCGCT GACCATAGA TCCTGCGCGT GACCATAGA TCCTGCGCGT GACCATAGA TCCTGCGCGCT GACCATAGA TCCTGCGCGT GACCATAGA TCCTGCGCGT GACCATAGA TCCTGCGCGCT GACCATAGA TCCTGCGCGT GACCATAGA TCCTGCGCGT GACCATAGA TCCTGCGCGCGT GACCATAGA TCCTGCGCGCT GACCATAGA TCCTGCGCGT GACCATAGA TCCTGCGCGT GACCATAGA TCCTGCGCGCT GACCATAGA TCCTGCGCTGCT GACCATAGA TCCTGCGCGCT GACCATAGA TCCTGCGCGCT GACCATAGA TCCTGCGCTGCT GACCATAGA TCCTGCGCTGCT GACCATAGA TCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
3244	AAGGAGGGCT ACGGCGAGGG CTGCGTGACC ATCCACGAGA TCGAGAACAA CACCGAGAACAA CACCACGAGAACAA CACCGAGAACAA CACCACGAACAA CACCGAACAA CACCACAACAA CACCACAACAA CACCACAACA
3304	CTGAAGTTCA AGAACCGCGA GGAGGAGGAG GTGTACCCCA CCGACACCGG CACCTGCAAC LeuLysPhe LysAsnArg GluGluGluGlu ValTyrPro ThrAspThr GlyThrCysAsn
3364	GACTACACCG CCCACCAGGG CACCGCCGGC TGCGCCGACG CCTGCAACAG CCGCAACGCC GACTACACCG CCCACCAGGG CACCGCCGGC TGCGCCGACG CCTGCAACAG CCCACCTAC ASpTyrThr AlaHisGln GlyThrAlaGly CysAlaAsp AlaCysAsn ScrArgAsnAla
3424	AspTyrThr Alahisdin GlyThinddol Transparence Accordage TGAACTACAA GCCCACCTAC GGCTACGAGG ACGCCTACGA GGTGGACACC ACCGCCAGCG TGAACTACAA GCCCACCTACGA GCGCACCTACGA GCGCGGCTAC GLYTyrGlu AspAlaTyr GluValAspThr ThrAlaSer ValAsnTyr LysProThrTyr GlyTyrGlu AspAlaTyr GluValAspThr ThrAlaSer GCGACTACGA CCGCGGCTAC
3484	GlyTyrGlu AspAlatyr GluvalAspInt Introduction GCGAGTACGA CCGCGGCTAC GAGGAGGAGA CCTACACCGA CGTGCGCCGC GACAACCACT GCGAGTACGA CCGCGGCTAC GAGGAGGAGA CCTACACCGAG AspAsnHis CysGluTyr AspArgGlyTyr GluGluGlu ThrTyrThr AspValArgArg AspAsnHis CysGluTyr CTTCCCGAG
3544	GluGluGlu ThrTyrThr AspvalArgary Asproximes of GluGluGluGlu ThrTyrThr AspvalArgary Asproximes of GluGluGluGluGluGluGluGluGluGluGluGluGluG
	ValAsnTyr ProProVal ProAlaGlyTyr ValInibys Grabeth ProAlaGlyTyr ValInibys Grabeth ProProVal ProAlaGlyTyr ValInibys Grabeth ProProVal ProAlaGlyTyr ValInibys Grabeth ProAlaGlyTyr ValInibys Grabeth ProProVal ACCGACACCG TGTGGATCGA GATCGGCGAG ACCGAGGGCA AGTTCATCGT GGACAGCGTG ACCGACACCG TGTGGATCGAT GATCAGCGTG GACAGCGTG ACCGACACCG TGTGGATCGATCGATCGATCGATCGATCGATCGATCGATC
3604	ThrAspThr ValTrpIle GluIleGlyGlu ThrGluGly Lysthelic Vallapor
3664	GAGCTGCTGC TGATGGAGGA GTAG GluLeuLeu LeuMetGlu Glu

Fig. 7A

SEQUENCE OF THE FULL-LENGTH HYBRID SYNTHETIC/NATIVE CRYIA(B) CHIMERIC GENE The fusion point between the synthetic and native coding sequences is indicated by a slash (/) in the sequence.

	by a slash (/) in the sequence.
1	ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG
	GTGGAGGTGC TGGGCGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CATCAGCCTG
121	AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG
181	GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGAIC
241	GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCCTG Cluclplou lleAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla IleSerArgLeu
301	GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC
361	CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC
421	CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG CTGACCACCG CCATCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG CTGACCACCG CCATCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG CTGACCACCG CCATCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCCT GCTGAGCGTG CTGACCTACCT GTTCGCCGTG CAGAACTACC AGGTGCCCCCT GCTGAGCGTG CTGACCTACTACTACTACTACTACTACTACTACTACTACTACT
481	TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCGA ACGTCAGCGT GTTCGGCCAG TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCGA ACGTCAGCGT GTTCGGCCAG TACGTGCAGG CCGCAACCT GCACCTGAGC GTGCTGCAGCGT GTTCGGCCAG TACGTGCAGG CCGCAACCT GCACCTGAGC GTGCTGCAGCAG ACGTCAGCGT GTTCGGCCAG TACGTGCAGCAGAGC GTGCTGCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGA
541	CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATO
601	GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGGT GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGGGT GGCAACTACA CACACACCACGC CGTGCGAGCG TACAACACCG GCCTGGAGCG CGTGTGGGGGGT GGCAACTACA CACACACCACGC CGTGCGAGCG CGTGTGGGGGGGCG CGTGGGGGGGGGG
661	CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCIGACCGIC
721	CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAI CCGCACCGIA
781	AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTICGA CGCCAGCTPA
841	CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCGTG CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCGTG CGCGGCAGCG CCCACCTGAT GGACATCGTG CGCGCACCTGAT CCCACCTGATCGTG CGCGCACCTGATCGTG CGCGCACCTGATCGTG CGCGCACCTGATCGTG CGCGCACCTGATCGTG CGCACCTGATCGTG CGCACTGATCGTG CGCACTGATCTGAT
901	CCAMCON CAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGCCCAC

Fig. 7B

961	ATCATGGCCA GCCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr
1021	ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC
1081	ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
1141	AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG AGCGTGCTGG ACGGCACCAGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG AGCGTGCTGCACAGA GCAACCTGCC CAGCGCCGTGCAGAGA GCAACCTGCC CAGCGCCGTGCAGAGACAGAGAGAGAGAGAGAGAGAGAACAGAGAGAG
1201	TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGAACTACAACTACGAACTACAACTACGAACTACAACTACGAACTACAACA
1261	CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC
1321	AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGGG AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGGGATTCA CCGCAGTGGATTCA CCGCAGTGATTCA CCGAGTGATTCA CCGAGTGATTCA CCGAGTGATTCA CCGAGTGATTCA CCGAGTGATTCA CCGAGTGATTCA CCAGTGATTCA CCGAGTGATTCA CCGAGTGATTCA CCGAGTGATTCA CCGAGTGATTCA CCGAGTGATTCA CCGA
1381	GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC GLUPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr
1441	AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG AACCTGGGCA GCGCCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG AACCTGGGCA GCGCCACAGAGC AACCTGGGCA GCGCCAGAGC
1501	AsnLeuGly Sergiythr Servarvatily of Caracterian Sergiythr Servarvatily of Caracterian Acatemical Coccession of Caracterian Caracterian Sergitary Servary Caracterian Servary Caracterian C
	Argardin Selflodly Cimilary
1561	GlnArgTyr ArgvalArg Tichtg-Tichtg-Tichtg-Tichtg-Carc CGCCAGCAC
1621	IleAspGly ArgProlle AshGlholymor
1681	LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsh FHESEIMSHOLY
1741	AGCAGCGTGT TCACCCTGAS SerAlaHisVal PheAsnSer GlyAshGlu VallyTTEAGE SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAshGlu VallyTTEAGE SERAGAGGGCT
1801	ArgileGlu Phevaipio Alacidatalia
1861	ArglleGlu Phevalflo Ardolava L CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal

Fig. 7C

1921	ACCGACTACC ACATCGAT/CA AGTATCCAAT TTAGTTGAGT GTTTATCTGATGAATTTTGT ThrAspTyr HislleAsp/GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys
1981	CTGGATGAAA AAAAAGAATT GTCCGAGAAA GTCAAACATG CGAAGCGACT TAGTGATGAG
2041	CGGAATTTAC TTCAAGATCC AAACTTTAGA GGGATCAATA GACAACTAGA CCGIGGCIGG
2101	AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTA
2161	ACGCTATTGG GTACCTTTGA TGAGTGCTAT CCAACGTATT TATATCAAAA AATAGATGAA
2221	TCGAAATTAA AAGCCTATAC CCGTTACCAA TTAAGAGGGT ATATCGAAGA TAGTCAAGA
2281	TTAGAAATCT ATTTAATTCG CTACAATGCC AAACACGAAA CAGTAAATGT GCCAGGTACG
2341	GGTTCCTTAT GGCCGCTTTC AGCCCCAAGT CCAATCGGAA AATGIGCCCA ICATIOSHIS
2401	CATTTCTCCT TGGACATTGA TGTTGGATGT ACAGACTTAA ATGAGGACTT AGGTGTATGG HisPheSer LeuAsplle AspValGlyCys ThrAspLeu AsnGluAsp LeuGlyValTrp
2461	HisPheSer LeuAspile Aspvalotyojo transpersion in the Agametration of the Agametratical
	Valilerne Lysitelys information
2521	GluGluLys ProLeuval Gryotanian
2581	Argasplys Arguidlys heddrard
2641	TCTGTAGATG TILLIAN Phe ValAsnSerGln TyrAspArg LeuGINAIA ASPINIANTE
2701	GCGATGATTC ATGCGGCAGA TAAACGCGTT CATAGCATTC GAGAAGCIIA ICIGGGGAGAGCIIA ICIGGGGAAGCIIA ICIGGGGAAGCIIA ICIGGGGAGAGCIIA ICIGGGGAAGCIIA ICIGGGAAGCIIA ICIGGAAGCIIA ICIGGAAACCIIA ICIGGAAACCII
2761	CTGTCTGTGA TTCCGGGTGT CAATGCGGCT ATTTTTGAAG AATTAGAAGG GCGTATTTTGAAG AATTAGAAGG GCGTATTTTTGAAG AATTAGAAGG GCGTATTTTTGAAG AATTAGAAGG GCGTATTTTTTGAAG AATTAGAAGG GCGTATTTTTTTTTT
2821	GCGDATATICA TCCCAGAAAT GTCATTAAAA ATGGTGAIII MAAAAAAA AAGGTGAIII MAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Fig. 7D

2881	TTATCCTGCT GGAACGTGAA AGGGCATGTA (LeuSerCys TrpAsnVal LysGlyHisVal R	upharer officer
2941	GTCCTTGTTG TTCCGGAATG GGAAGCAGAA (ValleuVal ValProGlu TrpGluAlaGlu	GTGTCACAAG AAGTTCGTGT CTGTCCGGGT ValSerGln GluValArg ValCysProGly
3001	CGTGGCTATA TCCTTCGTGT CACAGCGTAC	AAGGAGGGAT ATGGAGAAGG TTGCGTAACC LysGluGly TyrGlyGlu GlyCysValThr
3061	ATTCATGAGA TCGAGAACAA TACAGACGAA	CTGAAGTTTA GCAACTGTGT AGAAGAGGAA LeuLysPhe SerAsnCys ValGluGluGlu
3121	GTATATCCAA ACAACACGGT AACGTGTAAT ValTyrPro AsnAsnThr ValThrCysAsn	CARRADA CHIC CCACTCAACA AGAATATGAG
3181		GACGGAGCCT ATGAAAGCAA TTCTTCTGTA AspGlyAla TyrGluSer AsnSerSerVal
3241		AAAGCATATA CAGATGGACG AAGAGACAAT LysAlaTyr ThrAspGly ArgArgAspAsn
3301		TACACACCAC TACCAGCTGG CTATGTGACA TyrThrPro LeuProAla GlyTyrValThr
3361	AAAGAATTAG AGTACTTCCC AGAAACCGAT LysGluLeu GluTyrPhe ProGluThrAsp	AAGGTATGGA TTGAGATCGG AGAAACGGAA LysValTrp IleGluIle GlyGluThrGlu
3421	GGAACATTCA TCGTGGACAG CGTGGAATTA GlyThrPhe IleValAsp SerValGluLeu	CTTCTTATGG AGGAATAA LeuLeuMet GluGlu

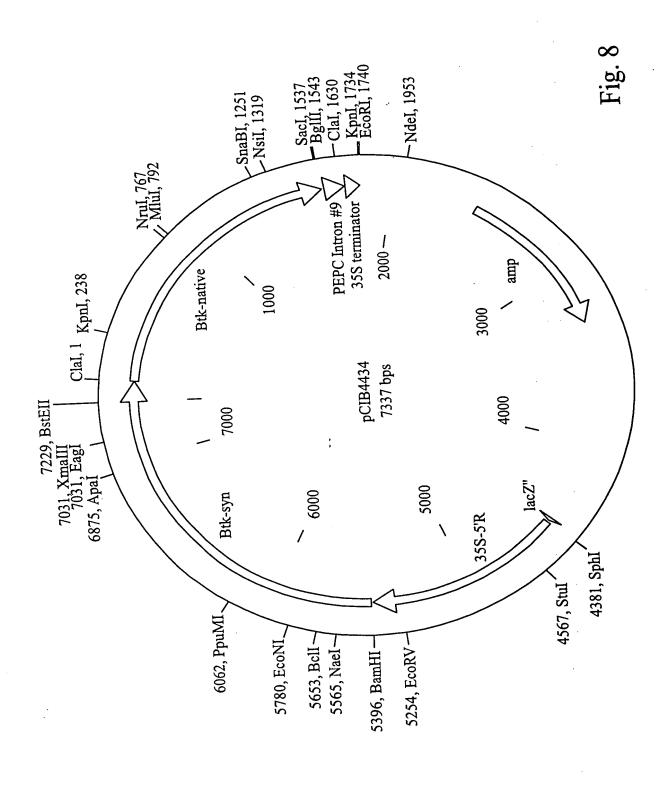


Fig. 9A

1.6.
1 ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu
61 GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CATCAGCCTG ValGluVal LeuGlyGly GluArgIleGlu ThrGlyTyr ThrProIle AspIleSerLeu
121 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG SerLeuThr GlnPheLeu LeuSerGluPhe ValProGly AlaGlyPhe ValLeuGlyLeu
181 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnIle
241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCCTG
301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAC GluGlyLeu SerAsnLeu TyrGlnIleTyr AlaGluSer PheArgGlu TrpGluAlaAsp
361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGCGCC ProThrAsn ProAlaLeu ArgGluGluMet ArgIleGln PheAsnAsp MetAsnSerAla
421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG
481 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTCGGCCAG TyrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGlyGln
541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC ArgTrpGly PheAspAla AlaThrIleAsn SerArgTyr AsnAspLeu ThrArgLeuIle
601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly
661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG ProAspSer ArgAspTrp IleArgTyrAsn GlnPheArg ArgGluLeu ThrLeuThrVal
721 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCCAT CCGCACCGTG
781 AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
841 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCACCTGAT GGACATCCTG
901 AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACCAG
961 ATCATGGCCA GCCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGGCACC IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr
·

Fig. 9B

- 1021 ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg
- 1081 ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG ThrLeuSer SerThrLeu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu
- 1141 AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG SerValLeu AspGlyThr GluPheAlaTyr GlyThrSer SerAsnLeu ProSerAlaVal
- 1201 TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal
- 1261 CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC ProProArg GlnGlyPhe SerHisArgLeu SerHisVal SerMetPhe ArgSerGlyPhe
- 1321 AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla
- 1381 GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC GluPheAsn AsnIleIle ProSerSerGln IleThrGln IleProLeu ThrLysSerThr
- 1441 AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG AsnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu
- 1501 CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCTGAGC ArgArgThr SerProGly GlnIleSerThr LeuArgVal AsnIleThr AlaProLeuSer
- 1561 CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGTT CCACACCAGC GlnArgTyr ArgValArg IleArgTyrAla SerThrThr AsnLeuGln PheHisThrSer
- 1621 ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGCAAC IleAspGly ArgProlle AsnGlnGlyAsn PheSerAla ThrMetSer SerGlySerAsn
- 1681 CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT CAGCAACGGC LeuGlnSer GlySerPhe ArgThrValGly PheThrThr ProPheAsn PheSerAsnGly
- 1741 AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACATCGAC SerSerVal PheThrLeu SerAlaHisVal PheAsnSer GlyAsnGlu ValTyrIleAsp
- 1801 CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCT GGAGAGGGCT ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla
- 1861 CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA TCGGCCTGAA GACCGACGTG GlnLysAla ValAsnGlu LeuPheThrSer SerAsnGln IleGlyLeu LysThrAspVal
- 1921 ACCGACTACC ACATCGATCA AGTATCCAAT TTAGTTGAGT GTTTATCTGA TGAATTTTGT ThrAspTyr HislleAsp GlnValSerAsn LeuValGlu CysLeuSer AspGluPheCys
- 1981 CTGGATGAAA AAAAAGAATT GTCCGAGAAA GTCAAACATG CGAAGCGACT TAGTGATGAG LeuAspGlu LysLysGlu LeuSerGluLys ValLysHis AlaLysArg LeuSerAspGlu

Fig. 9C

- 2041 CGGAATTTAC TTCAAGATCC AAACTTTAGA GGGATCAATA GACAACTAGA CCGTGGCTGG ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp
- 2101 AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTT ArgGlySer ThrAspIle ThrIleGlnGly GlyAspAsp ValPheLys GluAsnTyrVal
- 2161 ACGCTATTGG GTACCTTCGA CGAGTGCTAC CCCACCTACC TGTACCAGAA GATCGACGAG ThrLeuLeu GlyThrPhe AspGluCysTyr ProThrTyr LeuTyrGln LysIleAspGlu
- 2221 AGCAAGCTGA AGGCCTACAC CCGCTACCAG CTGCGCGGCT ACATCGAGGA CAGCCAGGAC SerLysLeu LysAlaTyr ThrArgTyrGln LeuArgGly TyrIleGlu AspSerGlnAsp
- 2281 CTGGAAATCT ACCTGATCCG CTACAACGCC AAGCACGAGA CCGTGAACGT GCCCGGCACC LeuGluIle TyrLeuIle ArgTyrAsnAla LysHisGlu ThrValAsn ValProGlyThr
- 2341 GGCAGCCTGT GGCCCCTGAG CGCCCCCAGC CCCATCGGCA AGTGCGGGGA GCCGAATCGA GlySerLeu TrpProLeu SerAlaProSer ProIleGly LysCysGly GluProAsnArg
- 2401 TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAG CysAlaPro HisLeuGlu TrpAsnProAsp LeuAspCys SerCysArg AspGlyGluLys
- 2461 TGCGCCCACC ACAGCCACCA CTTCAGCCTG GACATCGACG TGGGCTGCAC CGACCTGAAC CysAlaHis HisSerHis HisPheSerLeu AspIleAsp ValGlyCys ThrAspLeuAsn
- 2521 GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCA CGCCCGCCTG GluAspLeu GlyValTrp ValllePheLys IleLysThr GlnAspGly HisAlaArgLeu
- 2581 GGCAATCTAG AATTTCTCGA AGAGAAACCA TTAGTAGGAG AAGCACTAGC TCGTGTGAAA GlyAsnLeu GluPheLeu GluGluLysPro LeuValGly GluAlaLeu AlaArgValLys
- 2641 AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT ArgAlaGlu LysLysTrp ArgAspLysArg GluLysLeu GluTrpGlu ThrAsnIleVal
- 2701 TATAAAGAGG CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATAGATTA TyrLysGlu AlaLysGlu SerValAspAla LeuPheVal AsnSerGln TyrAspArgLeu
- 2761 CAAGCGGATA CCAACATCGC GATGATTCAT GCGGCAGATA AACGCGTTCA TAGCATTCGA GlnAlaAsp ThrAsnIle AlaMetIleHis AlaAlaAsp LysArgVal HisSerIleArg
- 2821 GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA GluAlaTyr LeuProGlu LeuSerValIle ProGlyVal AsnAlaAla IlePheGluGlu
- 2881 TTAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATG CGAGAAATGT CATTAAAAAT LeuGluGly ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValIleLysAsn
- 2941 GGTGATTTTA ATAATGGCTT ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA GlyAspPhe AsnAsnGly LeuSerCysTrp AsnValLys GlyHisVal AspValGluGlu
- 3001 CAAAACAACC ACCGTTCGGT CCTTGTTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA GlnAsnAsn HisArgSer ValLeuValVal ProGluTrp GluAlaGlu ValSerGlnGlu

Fig. 9D

- 3061 GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCGTGTCA CAGCGTACAA GGAGGGATAT ValArgVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr
- 3121 GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA CAGACGAACT GAAGTTTAGC GlyGluGly CysValThr IleHisGluIle GluAsnAsn ThrAspGlu LeuLysPheSer
- 3181 AACTGTGTAG AAGAGGAAGT ATATCCAAAC AACACGGTAA CGTGTAATGA TTATACTGCG AsnCysVal GluGluGlu ValTyrProAsn AsnThrVal ThrCysAsn AspTyrThrAla
- 3241 ACTCAAGAAG AATATGAGGG TACGTACACT TCTCGTAATC GAGGATATGA CGGAGCCTAT ThrGlnGlu GluTyrGlu GlyThrTyrThr SerArgAsn ArgGlyTyr AspGlyAlaTyr
- 3301 GAAAGCAATT CTTCTGTACC AGCTGATTAT GCATCAGCCT ATGAAGAAAA AGCATATACA GluSerAsn SerSerVal ProAlaAspTyr AlaSerAla TyrGluGlu LysAlaTyrThr
- 3361 GATGGACGAA GAGACAATCC TTGTGAATCT AACAGAGGAT ATGGGGATTA CACACCACTA AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu
- 3421 CCAGCTGGCT ATGTGACAAA AGAATTAGAG TACTTCCCAG AAACCGATAA GGTATGGATT ProAlaGly TyrValThr LysGluLeuGlu TyrPhePro GluThrAsp LysValTrpIle
- 3481 GAGATCGGAG AAACGGAAGG AACATTCATC GTGGACAGCG TGGAATTACT TCTTATGGAG GluIleGly GluThrGlu GlyThrPheIle ValAspSer ValGluLeu LeuLeuMetGlu
- 3541 GAATAA Glu---

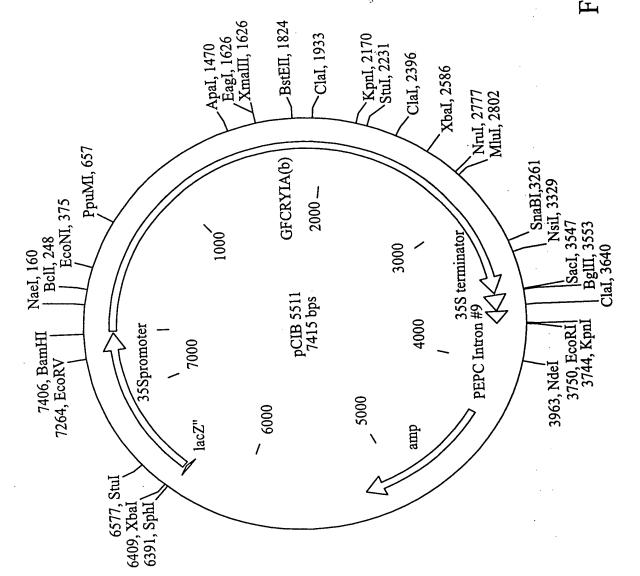


Fig. 10

Fig. 11A

1	ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu
61	GTGGAGGTGC TGGGCGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CATCAGGGTGC GTGGAGGTGC TGGGCGCGAGGAGGTGCATCGAGGTGCAGGGTGCAGGAGGTGCAGGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
121	AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTCGT GCTGGGCCTCGT GCTGGGGCCTCGT GCTGGGCCTCGT GCTGGGGCCTCGT GCTGGGGCCTGGGGCCTGGGGCCTGGGGCCTGGGGCCTGGGGCCTGGGGCCTGGGGGCCTGGGGGCCTGGGGGCCTGGGGGG
181	GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTGGT GUVALGINILE
241	GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAI CAGGGGGAG GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAI CAGGGGCAI CAGGGGCAI CAGGGCCAI CAGGCCAI CAGGGCCAI CAGGCCAI CAGGCCAI CAGGGCCAI CAGGCCAI CAG
301	GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG COAGAIG GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG COAGAIG GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG COAGAIG GCAACTGTACATCACACTGTACACTACACTGTACACACTACACTACACACTACACACTACACACTACACACTACACACTACACACTACACACTAC
361	CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GARGASSERALa
421	CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGIGCCCT LeuLeuSerVal
481	TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GIPHOGIYGIN
541	CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CONTROL
601	GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTTPGTy
661	CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC COTATALLANGTYRASD GLDPheArg ArgGluLeu ThrLeuThrVal
721	CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACGGACATCA TAGAGTATA CONTROL PROPERTY ASPSERARG THRTYPPRO IleArgThrVal
781	AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTICGA CGCGAGAT TTACACCAAC CCCGTGCTGG AGAACTICGA CGCGAGAT TACACCAAC CCCGAGAT TACACCAAC CCCAACACACACACACACACACACACA
843	CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCCAGGGCAGCA MetAspIleLeu
90	1 AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGI ACIACIGON AsnSerIle ThrIleTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHisGln
96	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

Fig. 11B

	The same of the sa
1021	ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg
1081	ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGGAGATAACAA CCAGCAGGAGAGAACAA CCAGCAGGAGAACAA CCAGCAGGAGAACAA CCAGCAGGAGAACAA CCAGCAGGAGAACAA CCAGCAGGAGAACAA CCAGCAGAGAACAA CCAGCAGAGAACAA CCAGCAGAACAA CCACACAACAAA CCAGCAGAACAAA CCAGCAGAACAAA CCAGCAGAACAAA CCAGCAGAACAAAAAAAA
1141	AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGGGCCGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG
1201	TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG TACCGCAAGA GCGCCACCGTGGCTTC
1201	TyrArgLys SelGlyIII Vallage
1261	Proproarg Ginglyine both proproarg GCCCAGTGCC
1321	ProProArg GINGIPPHE SETHIOMEGED AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA CCGCAGTGCC AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCAGAGCACC SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle HisArgSerAla SerAsnSer SerValSer IleIleArgAla ProMetPhe SerTrpIle CAAGAGCACC
1381	GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC OMITS OF THE PROSE OF THE PR
1441	AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG SASPILELEU
1501	CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC COORDING CONTROL CONTRO
1561	CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCIGCAGII SOLL CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCIGCAGII SOLL CAGCGCTACGC AGCACCACCA ACCIGCAGII SOLL CAGCGCTACGCA ACCIGCAGII SOLL CAGCGCTACGCA ACCIGCAGII SOLL CAGCGCTACGCA ACCIGCAGII SOLL CAGCGCTACCACCA ACCIGCAGII SOLL CAGCGCTACGCA ACCIGCAGII SOLL CAGCACCACCA ACCIGCAGII SOLL CAGCACCACCACCA ACCIGCAGII SOLL CAGCACCACCACCA ACCIGCAGII SOLL CAGCACCACCACCA ACCIGCAGII SOLL CAGCACCACCACCA ACCIGCAGII SOLL CAGCACCACCACCACCA ACCIGCAGII SOLL CAGCACCACCACCACCACCACCACCACCACCACCACCACC
1621	ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGGAG GGGCAS ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCCA CCATGAGGCAG GGGCAS ATCGAGGGCAG GGGCAGAGAGAGAGAGAGAGAGAGAGAGAG
1683	CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTT ON
174	1 AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT ValTyrIleAsp
-	SerServal Phethilica Soldan CCACAGGGCT
180	Argliediu Phevallio Marcha Cacceacha Cacceacha Cacceacha
186	GlnLysAla ValAshGld Booth
192	ACCGACTACC ACATCGATCA GGTGAGCAAC CTGGTGGAGT GGTTAAGGCTAACCTACCTACAACA
198	ACAACCACCT GAGCGAGAAG GTGAAGCACG CCAAGCATAG LeuSerAspGlu
:	

Fig. 11C

	CGCAACCTGC TGCAGGACCC CAACTTCCGC GGCATCAACC GCCAGCTGGA CCGCGGCTGG CGCAACCTGC TGCAGACTACAACC GCCAGCTGGA CCGCGGCTGG CGCAACCTGC TGCAGACTACAACC GCCAGCTGGA CCGCGGCTGGA CGCAACCTGC TGCAGACTTCCGC GGCATCAACC GCCAGCTGGA CCGCGGCTGGA CGCAACCTGC TGCAGACTACAACC GCCAGCTGGA CCGCAGCTGGA CCGCGGCTGGA CCGCAGCTGAACAACAACAACAACAACAACAACAACAACAACAACAAC
2041	CGCAACCTGC TGCAGGACCC CAACTTCCGC GGCATCAACC GCCAGCTGGA CCGCGGGTCP ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnCG TGTTCAAGGA GAACTACGTG
2101	CGAGGCAGCA CCGATATCAC CATCCAGGGC GGCGACGACG IGITCANGOLOGICA CCGATATCAC CATCCAGGGC GGCGACGACG IGITCANGOLOGICA CONTROL CATCCAGGGC GACGACGACG IGITCANGOLOGICA CONTROL CATCCAGGGC GACGACGACG GACGACGACG GACGACGACG GACGACGACG GACGACGACGACG GACGACGACGACGACGACGACGACGACGACGACGACGACG
2161	ACCCTGCTGG GCACCTTCGA CGAGTGCTAC CCCACCTACC TGTACCAGAA GIACAGAA GAGTGCTAC CCCACCTACC TGTACCAGAA GIACAGAA GAGTGCTAC CCCACCTACC TGTACCAGAA GAGTGCTAC CCCACCTACC TGTACCAGAA GAGTGCTAC TGTACAGAA GAGTGCTAC TGTACAGAA GAGTGCTAC TGTACAGAA GAGTGCTAC TGTACAGAA GAGTGCTAC TGTACAGAA GAGTGCTAC TGTACAGAA GAGTACAGAA GAGTACAGAAA GAGTACAGAA GAGTACAGAA GAGTACAGAA GAGTACAGAA GAGTACAGAA GAGTACAGAA GAGTACAGAA GAGTACAGAA GAGTACAGAA GAGTACAGAAA GAGTACAGAA GAGTACAGAAA GAGAAA GAGAAA GAGTACAGAA GAGTACAGAA GAGTACAGAA GAGTACAGAAA
2221	AGCAAGCTGA AGGCCTACAC CCGCTACCAG CTGCGGGGCI AGAIOGIU AspSerGlnAsp
2281	CTGGAAATCT ACCTGATCCG CTACAACGCC AAGCACGAGA CCGTGATAC ValProGlyThr
2341	GGCAGCCTGT GGCCCCTGAG CGCCCCCAGC CCCATCGGCT TO AGE GOVERNARY
2401	TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGGAGG AspGlyGluLys
2461	TCCCCCCACC ACAGCCACCA CTTCAGCCTG GACATCGACG TOOLS ThrAspLeuAsn
2521	GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCO MOONASPGLY HisAlaArgLeu
2581	GluAspleu GlyVdliff GluAspleu GlyVdliff GCCAATCTAG AATTTCTCGA AGAGAAACCA TTAGTAGGAG AAGCACTAGC TCGTGTGAAA LeuValGly GluAlaLeu AlaArgValLys
264	GIYASHLEU GIUTHOLO 1 AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT 1 AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT 1 AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATTGTT
270	Argalagiu hysbyster some Argalagiu hysbyster s
210	TUY LVSGIU ALOUY OUT THE CONTROL GA
276	CINALAASD IIIIMSHIII mmmmchagaa
282	Clublator Leuricora Dona Charly Vy Val
288	TTAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATO TAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATO ALAUGIUGIV ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValileLysAsn LeuGluGlv ArgIlePhe ThrAlaPheSer LeuTyrAsp AlaArgAsn ValileLysAsn
29	41 GGTGATTTTA ATAATGGCTT ATCCTGCTGG AACGTGAAAG GGGTAAGGAAAG ASPVALGIUGIU
30	ACCOMPAGE COTTGTTGTT COGRAM COLINIAGIU ValSerGINGIU

Fig. 11D

3061	GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCGTGTCA CAGCGTACAA GGAGGGATAT ValargVal CysProGly ArgGlyTyrile LeuArgVal ThralaTyr LysGluGlyTyr
3121	ValargVal CysProGly ArgGlyTyTTD GAGAACAATA CAGACGAACT GAAGTTTAGC GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA CAGACGAACT GAAGTTTAGC GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA CAGACGAACT GAAGTTTAGC GGAGAAGGTT GCGTAATGA TTATACTGCG
	GlyGluGly Cysvalini Figure 6 Commanda TTATACTGCG
3181	AshCysVal Gludiudiu Valli
3241	ThrGInGlu GluiyiGiu Giji
3301	GluSerAsn Seiseival Floridati I
3361	GluSerAsn SerServal FloAranopy/ GATGGACGAA GAGACAATCC TTGTGAATCT AACAGAGGAT ATGGGGATTA CACACCACTA GATGGACGAA GAGACAATCC TTGTGAATCT AACAGAGGAT ATGGGGATTA CACACCACTA AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly TyrGlyAsp TyrThrProLeu AspGlyArg ArgAspAsn ProCysGluSer AsnArgGly AAACCGATAA GGTATGGATT
3421	CCAGCTGGCT ATGTGACAAA AGAATTAGAG TACTTCCCAG AAACCGATATTCCCAG AAACCGATATTCCAGACGATATTCCCAG AAACCGATATTCCCAG AAACCGATATTCCAGACAGACGATATTCCAGACAGACAGA
3481	TARGERIC ANACGGAAGG AACATTCATC GTGGACAGCG IGGAATHALEU LeuLeuMetGlu
•	GluIleGly GluIniGlu Glyland
3541	GAATAA Glu

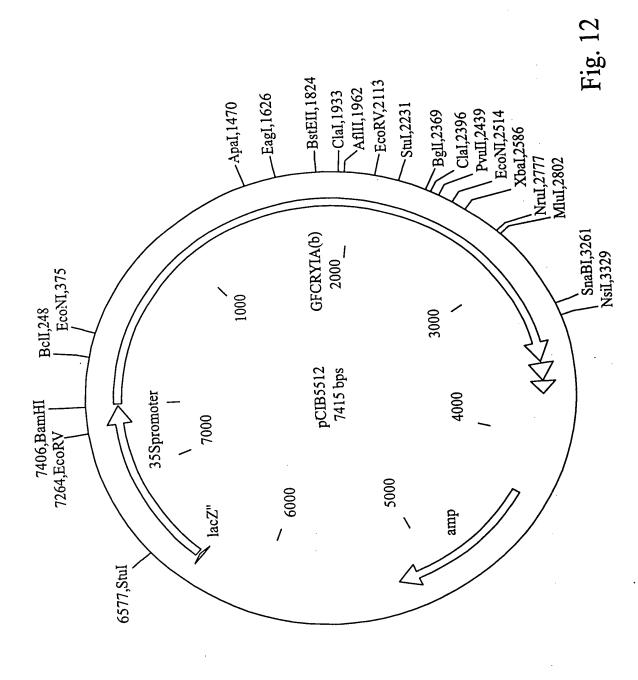


Fig. 13A

1	ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG MetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu
61	GTGGAGGTGC TGGGCGGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CAICAGCCTG
121	AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGCCTG
181	GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGATC
241	GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCCTG GAGCAGCTGA TCAACCAGCCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCCTG GAGCAGCTGA TCAACCAGCCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCCTG GAGCAGCTGA TCAACCAGCCAT CAGCCGCTG GAGCAGCTGA TCAACCAGCCAT CAGCCGCTG GAGCAGCCAT CAGCCGCTG GAGCAGCTGA TCAACCAGGCCAT CAGCCGCTGA GAGCAGCTGA TCAACCAGGCCAT CAGCCGCTGA GAGCAGCTGA TCAACCAGGCCAT CAGCCGCTGA GAGCAGCTGA TCAACCAGGCCAT CAGCCGCTGA GAGCAGCTGA TCAACCAGCTGA TCAACCAGCTGA TCAACCAGGCCAT CAGCCGCTGA GAGCAGCTGA TCAACCAGCTGA TCAACCAGCTGA TCAACCAGGCCAT CAGCCGCTGA TCAACCAGCTGA TCAACCAGCCAGACAACAACAACAACAACAACAACAACAAC
301	GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAAGCCCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAAGCCCAACCTGAACCTGAACCTACAACCTGAACCTACAACCTGAACACCTACAACCTACAACCTACAACACAACCTACAACAA
361	CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGGGGAGATG CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGGGGAGATG CCCACCAACC CCACCAACC CGAGGAGATG CGCATCCAGT TCAACGACAT GAACAGGGGAGATG CCCACCAACC
421	CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGACCACCT GCTGACACCT GCTGACACACCT GCTGACACACACACACACACACACACACACACACACACAC
481	TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTCAGCGT GTTGGGGCTACGTGCGCG ACGTCAGCGT GTTGGGGCG TACGTCAGCGT GTTGGGGCG ACGTCAGCGT GTTGGGGCG ACGTCAGCGT GTTGGGGCG ACGTCAGCGT GTTGGGCGT GTTGGGCGGCGT GTTGGGCGGCGT GTTGGGCGGCGT GTTGGGCGGCGGCGGCGGCGGGCG
541	CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC COORDINATED AND ALATHRILEASH SERARGTYR ASHASPLEU THRAFGLEUILE
601	GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGGG GGCAGCACTACA CACACACACGC GCCTGGAGGG GGCAGCACACACACACACACACACACACACACA
661	CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC GOLDAN GLORING CCCGACAGCT GCGAGCTGACAAC CAGTTCCGCC GCGAGCTGAC GCGAGCTGACAC GCAGACTGACAC GCAGACTAC GCAGACTAC GCACACACACACACACACACACACACACACACACACA
721	CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA CCTACCCOATTEATTAIN PheProAsnTyr AspSerArg ThrTyrPro IleArgThrVal
781	LeuAspile Valselled Thorotage CCCGTGCTGG AGAACTTCGA CGGCAGCTTC
841	SerginLeu Inflatgord 12019 SerginLeu Inflatgord
	ArgGlySer Alagingly 11002011
901	AshSerile initially initial
96:	1 ATCATGGCCA GCCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GIACGGAGT 1 IleMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGlyThr

Fig. 13B

1021	ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC MctGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg
1081	ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG The Louser SerThrleu TyrArgArgPro PheAsnIle GlyIleAsn AsnGlnGlnLeu
1141	AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCTGCC CAGCGCCGTG
1201	TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTO TACCGCAAGA CAACAACGTO TACCAGCAAGA CAACAACGTO TACCACAAGA CAACAACGTO TACCAGCAAGA CAACAACGTO TACCAGCAAGA CAACAACGTO TACCAGCAAGATCC CCCCTCAGAA CAACAACGTO TACCAGCAAGATCC CCCCTCAGAACAACGTO TACCAGCAAGATCC CCCCTCAGAACAACAACAACGTO TACCAGCAAGATCC CCCCTCAGAACAACAACAACAACAACAACAACAACAACAACAACA
1261	CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCATGTTCCG CAGTGGCTTC CCACCTCGAC AGGGCTTCAG AGCCACGTGA GCATGTTCAG AGCCACGTGA AGCCACACGTGA AGCCACACGTGA AGCCACACGTGA AGCCACACACACACACACACACACACACACACACACA
1321	AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATICA CCGCAGTGGA
1381	GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC
1441	AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATOOTO AACCTGGGCA GCGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATOOTO AACCTGGGCA GCGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATOOTO AACCTGGGCA GCGCACATOOTO AACCTGGGCA GCGCACATOOTO AACCTGGGCACATOOTO AACCTGGCACATOOTO AACCTGGCACATOOTO AACCTGGCACATOOTO AACCTGGCACATOOTO AACCTGGCACATOOTO AACCTGGCACATOOTO AACCTGGCACATOOTO AACCTGGCACATOOTO AACCTGGCACATOOTO AACCTGCACATOOTO AACCTCCACATOOTO AACCTCCACA
1501	CGCCGCACCA GCCCCGGCCA GATCAGCACC CTGCGCGTGA ACATCACCGC CCCCGCGACA
1561	CAGCGCTACC GCGTCCGCAT CCGCTACGCC AGCACCACCA ACCTGCAGII CCACACOAGC
1621	ATCGACGGCC GCCCCATCAA CCAGGGCAAC TTCAGCGCCA CCATGAGCAG CGGCAGAAAAAAAAAA
1681	CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTI CAGCAACGG CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTI CAGCAACGG CTGCAGAGCG GCAGCTTCCG CACCGTGGGC TTCACCACCC CCTTCAACTI CAGCAACGG
1741	AGCAGCGTGT TCACCCTGAG CGCCCACGTG TTCAACAGCG GCAACGAGGT GTACHTONIA
1801	CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCI GGAGAGGGG L CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGACCI GGAGAGGGGCG
1863	1 CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA 1CGGCCTGAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA
192	1 ACCGACTACC ACATCGATCA GGTGAGCAAC CTGGTGGAGT GCTTAAGCGA COADUPHECYS
198	Thrasptyr Hisitonep of the Thrasptyr Hisitonep o
:	•

Fig. 13C

2041	CGCAACCTGC TGCAGGACCC CAACTTCCGC GGCATCAACC GCCAGCTGGA CCGCGGCTGG ArgAsnLeu LeuGlnAsp ProAsnPheArg GlyIleAsn ArgGlnLeu AspArgGlyTrp
2101	CGAGGCAGCA CCGATATCAC CATCCAGGGC GGCGACGACG TGTTCAAGGA GAACTACGTG
2161	ACCCTGCTGG GCACCTTCGA CGAGTGCTAC CCCACCTACC TGTACCAGAA GATCGACGAG
2221	AGCAAGCTGA AGGCCTACAC CCGCTACCAG CTGCGCGGCT ACATCGAGGA CAGCCAGGA
2281	CTGGAAATCT ACCTGATCCG CTACAACGCC AAGCACGAGA CCGTGAACGT GCCGGAACGT CTGGAAATCT ACCTGATCCG CTACAACGCC AAGCACGAGA CCGTGAACGT GCCGGAACGT GCCGGAACGT GCCGGAACGT GCCGGAACGT GCCGGAACGT GCCGAGACGT GCCGAGACGT GCCGGAACGT GCCGGAACGT GCCGAGAACGT GCCAGAACGT GCCAGAACGT GCCAGAACGT GCCAGAACGT GCCAGAACGAACAACGT GCCAGAACGAACAACGT GCCAGAACGT GCCAGAACGT GCCAGAACGT GCCAGAACGAACAACAACAACAACAACAACAACAACAACA
2341	GGCAGCCTGT GGCCCCTGAG CGCCCCCAGC CCCATCGGCA AGTGCGGGGA GCCGAATCAA
2401	TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAAC TGCGCTCCGC ACCTGGAGTG GAACCCCGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAACA TGCGCTCCGC ACCTGCAGGGAC CTAGACTGCA GCTGCAGGGA CGGGGAGAACA TGCGCTCCGC ACCTGCAGACTGCA GCTGCAGGGACAACA TGCGCTCCGCACACACACACACACACACACACACACACAC
2461	TGCGCCCACC ACAGCCACCA CTTCAGCCTG GACATCGACG TGGGCTGCAC CGACGTGATT TGCGCCCACC ACAGCCTG GACATCGACG TGGGCTGCAC CGACGTGATT TGCGCCCACCACCACCACACACACACACACACACACACAC
2521	GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCA CGCCGGGCA GLCCATTCD VallePheLys IleLysThr GlnAspGly HisAlaArgLeu
2581	GGCAATCTAG AGTTCCTGGA GGAGAAGCCC CTGGTGGGCG AGGCCCTGGC CCGGGTGATC
2641	CGCGCCGAGA AGAAGTGGCG CGACAAGCGC GAGAAGCTGG AGTGGGAGAC CAACATGGCGC CGACAGGCGC GAGAAGCTGG AGTGGGAGAC CAACATGGCGC GAGAAGCTGG AGTGGAGAGC CAACATGGCGC GAGAAGCTGG AGTGGAGAGC CAACATGGCGC GAGAAGCTGG AGTGGAGAC CAACATGGCGC GAGAAGCTGG GAGAAGCTGG AGTGGAGAGC CAACATGGCGC GAGAAGCTGG GAGAAGCTGGAGAGC CAACATGGCGC GAGAAGCTGGAGAGC CAACATGGCGC GAGAAGCTGGAGAGAC CAACATGGCGC GAGAAGCTGGAGAGC CAACATGGCGC GAGAAGCTGGAGAGAC CAACATGGAGAAGCTGGAGAGAC CAACATGGCGCAAGACTGAGAAGACTGAGAAGCTGAGAAGAAGCTGAGAAGAAGCTGAGAAGAAGCTGAAGAAGCTGAGAAGAAGCTGAGAAGAAGCTGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG
2701	TACAAGGAGG CCAAGGAGAG CGTGGACGCC CTGTTCGTGA ACAGCCAGTA CGAOOSTA
2761	CAGGCCGACA CCAACATCGC CATGATCCAC GCCGCCGACA AGCGCGIGCA CAGGATION CAGGCCGACA AGCGCGACA CAGCATION CAGGCCGACA CAGCATION
282	1 GAGGCCTACC TGCCCGAGCT GAGCGTGATC CCCGGCGTGA ACGCCGCCAT GITGGLUGIU
288	1 CTCGAGGGCC GCATCTTCAC CGCCTTCAGC CTGTACGACG CCCGCAACGT GATGALIAN AND CTCGAGGGCC GCATCTTCAC CGCCTTCAGC CTGTACGACG CCCGCAACGT GATGALIAN AND CTCGAGGGCC CCGCAACGT GATGALIAN AND CTCGAGGCC CTCGAGGCC CCGCAACGT GATGAGCC CTCGAGGCC CCGCAACGT GATGALIAN AND CTCGAGGCC CTCGAGACGT GATGAGCC CTCGAGACGT GATGAGCC CTCGAGACGT GATGACGT GATGAGCC CTCGAGACGT GATGACGT GATGACGT GATGACGT GATGAGCC CTCGAGACGT GATGACGT GATGAC
294	1 GGCGACTTCA ACAACGGCCT GAGCTGCTGG AACGTGAAGG GCCACGTGGAAGG GCCACGTGAAGG GCCACGTGAAGG GCCACGTGGAAGG GCCACGTGGAAGG GCCACGTGAAGG GCCACGTGAAGG GCCACGTGAAGG GCCACGTGAAGG GCCACGTGGAAGG GCCACGTGAAGG GCCACACGTGAAGG GCCACACGTGAAGA GCCACACACACACACACACACACACACACACACA
300	GlyAspPhe ASHASHGIY EGGGTGGTG CCCGAGTGGG AGGCCGAGGT GAGCCAGGAG

Fig. 13D

3061	GTGCGCGTGT GCCCCGGCCG CGGCTACATC CTGCGCGTGA CCGCCTACAA GGAGGGCTAC GTGCGCGTGT GCCCCGGCCG CGGCTACATC CTGCGCGTGA CCGCCCTACAA GGAGGGCTACAA ValargVal CysProGly ArgGlyTyrIle LeuArgVal ThrAlaTyr LysGluGlyTyr ValArgVal CysProGly ArgGlyTyrIle LeuArgVal CCGAGGAGGCT CAAGTTCAGC
3121	GGCGAGGGCT GCGTGACCAT CCACGAGATC GAGAACACA CCGACGAGGT GIMES CONTROL CO
3181	AACTGCGTGG AGGAGGAGGT GTACCCCAAC AACACCGTGA CCTGCAACGA CTACACCGTGA CACCGTGA CCTGCAACGA CTACACCGTGA AACACCGTGA AACACCGA AACACCGA AACACCACACACACACACA
3241	ACCCAGGAGG AGTACGAGGG CACCTACACC AGCCGCAACC GCGGCTACGA CGGGCTACGA CCCAGGAGG CACCTACACC AGCCGCAACC GCGGCTACGA CGGGCTACGA CGGGCTACGA CGGGCTACGA CGGGCTACGA CGGGCTACGA CGGGCTACGA CGGGCTACGA CGGCTACGA CGGGCTACGA CGGGCTACGA CGGCTACGA CGGCTACG
3301	GAGAGCAACA GCAGCGTGCC CGCCGACTAC GCCAGCGCCT ACGAGGAGAA GGCCTACTACTACTACTACTACTACTACTACTACTACTACTA
3361	GACGGCCGCC GCGACAACCC CTGCGAGAGC AACCGCGGCT ACGGCGACTA GAOGACTA GAOCACTA GAOGACTA GAOGACTA GAOGACTA GAOGACTA GAOGACTA GAOGACTA GAOGACTA GAOGACTA GAOCACTA GA
3421	AspGlyArg Argaspash Flooyouth CCCGCCGGCT ACGTGACCAA GGTGTGGATC CCCGCCGGCT ACGTGACCAA GGAGCTGGAG TACTTCCCCG AGACCGACAA GGTGTGGATC CCCGCCGGCT ACGTGACGACGATGGAG TACTTCCCCG AGACCGACAA GGTGTGGATCCCCGCCGATGGAGGAGACCGCCT ACGTGATGGAGGAGACCGCCT ACGTGATGGAGGAGACCGCCT ACGTGATGGAGAGACCGCCT ACGTGATGGAGAGACCGCCT ACGTGATGGAGAGACCGACGT ACGTGATGGAGAGAGACCGCCT ACGTGATGGAGAGACCGCCT ACGTGATGGAGAGACCT ACGTGATGGAGAGACCGCCT ACGTGATGGAGAGACCGCT ACGTGATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
	ProAlaGly Tyrvalini hysolubout 1
3481	GAGATCGCCG AGACCGAGGG CACCTTCATC GTGGACAGCG TGGAGCTGCT GCTGATACTCATC GTGGACAGCG TGGAGCTGCT GCTGATCATC GTGGACAGCG TGGAGCTGCT GCTGATCATCATCATCATCATCATCATCATCATCATCATCATCA
3541	GAG Glu

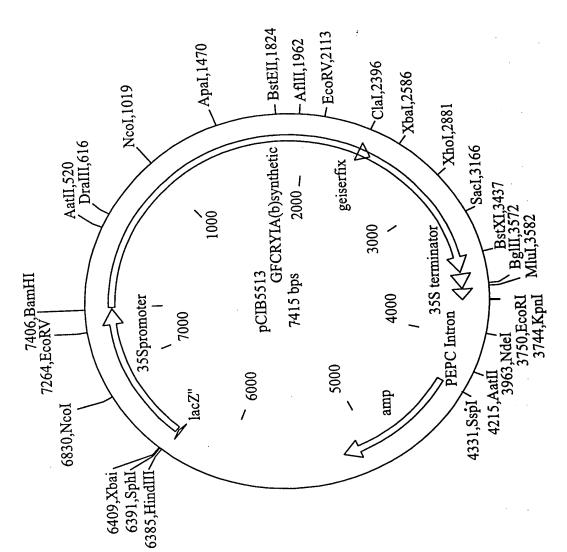


Fig. 14

Fig. 15A

1 ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACGAGTGC MetAspasn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGluCys I	eu TG eu TC le
AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCGT GCTGGGGC SerLeuThr GlnPheLeu LeuSerGluPhe ValP,roGly AlaGlyPhe ValLeuGlyL GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGTGCAGA ValAspIle IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnI	eu TC le TG
181 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTCGT CACCCGCC ValAspile IleTrpGly IlePheGlyPro SerGlnTrp AspAlaPhe LeuValGlnI	le тс
VALINOPTE TO THE COCCOCCA ACCACCCAT CAGCCGCC	eu
ValAspile Helipdiy Hothood 241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCCGCC 241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGAGTG GGAGGCCG GluGlnLeu HeAsnGln ArgIleGluGlu PheAlaArg AsnGlnAla HeSerArgI	
301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCGGCGAGAGCT TCGGAGAGCT TCGGAGAGAGCT TCGGAGAGAGCT TCGGAGAGAGCT TCGGAGAGAGCT TCGGAGAGAGCT TCGGAGAGAGCT TCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	sp
361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT	Ala
421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGIOOF LeuLeuSer	Val
481 TACGTGCAGG CCGCCAACCT GCACCTGAGC GTGCTGCGCG ACGTGAGG ValPheGly TvrValGln AlaAlaAsn LeuHisLeuSer ValLeuArg AspValSer ValPheGly	Gln ATC
541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGREGATION ThrangLeu ArgTrpGly PheAspAla AlaThrileAsn SerArgTyr AsnAspLeu ThrangLeu	Ile GGT
601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GGCTGGTG ArgValTrp	Gly 'CTG
661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGACGCULeu ThrLeuThi	Val CTG
721 CTGGACATCG TGAGCCTGTT CCCCAACTAC GACAGCCGCA GOTTYPPro IleArgTh: LeuAspIle ValSerLeu PheProAsnTyr AspSerArg ThrTyrPro IleArgTh:	CVAL
781 AGCCAGCTGA CCCGCGAGAT TTACACCAAC CCCGTGCTGG AGAINST ASPGLYSE SerGlnLeu ThrArgGlu IleTyrThrAsn ProValLeu GluAsnPhe AspGlySe	rPhe CCTG
841 CGCGGCAGCG CCCAGGGCAT CGAGGGCAGC ATCCGCAGCC CCGAGGCAGCC MetAspIl ArgGlySer AlaGlnGly IleGluGlySer IleArgSer ProHisLeu MetAspIl	eLeu CCAG
901 AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGI ACIACIONA AspSerlle ThrileTyr ThrAspAlaHis ArgGlyGlu TyrTyrTrp SerGlyHi	sGln
AsnSerIle ThrIleTyr ThrAspArants Mayorian AsnSerIle ThrIleTyr ThrAspArants Mayorian CTTCCCCCT GTACGO 961 ATCATGGCCA GCCCCGTCGG CTTCAGCGGC CCCGAGTTCA CCTTCCCCCT GTACGO 11eMetAla SerProVal GlyPheSerGly ProGluPhe ThrPhePro LeuTyrGl	yThr

Fig. 15B

1021	ATGGGCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg
1081	ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGGAGAACAA CCAGGAGAACAACAA CCAGGAGAACAAA CCAGGAGAACAAA CCAGGAGAACAAA CCAGGAGAACAAACA
1141	AGCGTGCTGG ACGGCACCGA GTTCGCCTAC GGCACCAGCA GCAACCAGCC CAGGGACCAGCA GCAACCAGCA CAGGGCACCAGCA GCAACCAGCA CAGGGCACCAGCA GCAACCAGCA CAGGGCACCAGCA GCAACCAGCA CAGGGCACCAGCA GCAACCAGCA CAGGGCACCAGCA GCAACCAGCA GCAACCAGCAGA GCAACCAGCAGA GCAACCAGCAGA GCAACCAGCAGA GCAACCAGCAGA GCAACCAGCAGA GCAACCAGCAGA GCAACCAGCAGCAACACAGCAGA GCAACCAGCAGA GCAACCAGACAGA
1201	TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAM SANASASASASASASASASASASASASASASASASASAS
1261	CCACCTCGAC AGGGCTTCAG CCACCGTCTG AGCCACGTGA GCAIGITCOS OS CONTROL CONTROL SERVICION SE
1321	AGCAACAGCA GCGTGAGCAT CATCCGTGCA CCTATGTTCA GCTGGATTCA GCTGATTCA G
1381	GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCTGAC CAAGAGCACC GAGTTCAACA ACATCATCCC CAGCAGCCAG ATCACCCAGA TCCCCCGCGG CGACATCCTG
1441	GluPheAsn AsnItelle Proserserorn and GCCCCGGCT TCACCGGCGG CGACATCCTG AACCTGGGCA GCGGCACCAG CGTGGTGAAG GGCCCCGGCT TCACCGGCGG CGACATCCTG ASnLeuGly SerGlyThr SerValValLys GlyProGly PheThrGly GlyAspIleLeu AsnLeuGly SerGlyThr SerValValLys GlyProGCCTGA ACATCACCGC CCCCCTGAGC
	AsnLeuGly Seldlylli Solver
1501	Argargini Selilodiy Santa
1561	GINARGTYF ALGVALATY TECHNOLOGIC CCCCAGCAGC
1621	Ileaspuly Algitoria and CACCAACGGC
1683	LeuGinser Gryseline Magazine LeuGinser Graca CCR CTACATCGAC
174	SerSerVal Phelifiled SerManner CARCAGGGCT
180	1 CGCATCGAGT TCGTGCCCGC CGAGGTGACC TTCGAGGCCG AGTACGAGG LeuGluArgAla ArgIleGlu PheValPro AlaGluValThr PheGluAla GluTyrAsp LeuGluArgAla
186	1 CAGAAGGCCG TGAACGAGCT GTTCACCAGC AGCAACCAGA 1CGGGGTU LysThrAspVal
192	1 ACCGACTACC ACATCGATCA AGTATCCAAT TTAGTIGAGT GITTAGTIGAGT ASPGLuPheCys
198	TOTAL ANANGIATT GTCCGAGAAA GTCAAACATT ALSINGARG LeuSerAspGlu

Fig. 15C

	CGGAATTTAC TTCAAGATCC AAACTTTAGA GGGATCAATA GACAACTAGA CCGTGGCTGG
2041	
2101	AGAGGAAGTA CGGATATTAC CATCCAAGGA GGCGATGACG TATTCAAAGA GAATTACGTA
2161	ACGCTATTGG GTACCTTTGA TGAGTGCTAT CCAACGTATT TATATCAAAA AATAGATGAGAAA ACGCTATTGG GTACCTTTGA TGAGTGCTAT CCAACGTATT TATATCAAAA AATAGATGAGAAAA AATAGATGAGAAAA AATAGATGAGAAAA AATAGATGAGAAAAAAAA
2221	TCGAAATTAA AAGCCTATAC CCGTTACCAA TTAAGAGGGT ATATCGARGA TTAAGAGGGGT ATATCGARGA TTAAGAGGGT ATATCGARGA TTAAGAGGGGT ATATCGARGA TTAAGAGGGT ATATCGARGA TTAAGAGGGGT ATATCGARGA TTAAGAGGGT ATATCGARGA TTAAGAGGGGT ATATCGARGA TTAAGAGGGGT ATATCGARGA TTAAGAGGGT ATATCGARGA TTAAGAGGGGT ATATCGARGA TTAAGAGAGGGT ATATCGARGAGGGT ATATCGARGAGGAGGT ATATCGARGAGGGT ATATCGARGAGGAGGGT ATATCGARGAGGAGGGT A
2281	TTAGAAATCT ATTTAATTCG CTACAATGCC AAACACGAAA CAGTAAATGT GCCAGGTTATTAGAAATCT ATTTAATTCG CTACAATGCC AAACACGAAA CAGTAAATGT GCCAGGTTATAGAAATCT ATTTAATTCG CTACAATGCC AAACACGAAA CAGTAAATGT GCCAGGTTATAGAAATCT GCCAGGTTATAGAATGT GCCAGGTTAGAATGT GCCAGGTTAGAATGTAGAATGTAGAATGTAGAATGTAGAATGTAGAATGTAGAATGTAGAATGTAGAATGTAGAATGTAGAATGTAG
2341	GGTTCCTTAT GGCCGCTTTC AGCCCCAAGT CCAATCGGCA AGTGCGGCA GIUProAsnArg
2401	TGCGCTCCGC ACCTGGAGTG GAACCCGGAC CTAGACTGCA GCTGCAGGGA COOLAGA TERASPROASP LeuAspCys SerCysArg AspGlyGluLys
2461	TGCGCCCACC ACAGCCACCA CTTCAGCCTG GACATCGACG TGGGCTGCAC TARASPLEUASN
2521	GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCH GALANGER GAGGACCTGG GCGTGTGGGT GATCTTCAAG ATCAAGACCC AGGACGGCCH GALANGER GAGGACGGCCH GALANGER GAGGACGGCCH GALANGER GAGGACGGCCH GAGGACGGCCH GALANGER GAGGACGGCCH GALANGER GAGGACGGCCH GAGGACGCCH GAGGACGCH GAGGACGGCCH GAGGACGGCCH GAGGACGCCH GAGGACGGCCH GAGGACGGCCH GAGGACGGCCH GAGGACGGCCH GAGGACGGCCH GAGGACGGCCH GAGGACGGCCH GAGGACGGCCH GAGGACGCCH GAGGACGCCH GAGGACGGCCH GAGGACGCCH GAGGACGCCH GAGGACGCCH GAGGACGCCH GAGGACGCH GAGGACGACH GAGGACGCH GAGGACGACH GAGACGACCH GAGGACGCH GAGGACGACH GAGACGACH GAGACGACCH GAGACGACGACH GAGACGACGACH GAGACGACGACH GAGACGACGACH GAGACGACGACH GAGACGACGACH GAGACGACGACH GAGACGACACH GAGACGACGACH GAGACGACH GAGACGACH GAGACGACH GAGACGACH GAGACACH GAGACGACH GAGACACH GACACH GAGACACH GAGACACH GAGACACH GACCACH GAGACACH GAGACACH GAGACACH GAGACACH GAGACACH GAGACA
2581	GGCAATCTAG AATTTCTCGA AGAGAAACCA TTAGTAGGAG AAGCACTAGG 100100000000000000000000000000000000
2641	AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC TAASATTAA AGAGCGGAGA AAAAATGGAG AGACAAACGT GAAAAATTGG AATGGGAAAC TAASATTAA AGAGCGGAAAC TAASATTAA AGAGCGAAAC TAASATTAA AGAGCGAAAC TAASATTAA AGAGCGAAAC TAASATTAA AGAGCGAAAC TAASATTAA AGAGCGAAAC TAASATTAA AGAGCGAAAC TAASATTAA AGAGCAAAC TAASATTAA AGAGCAAAC TAASATTAA AGAGCAAAC TAASATTAA AGAGCAAAAC TAASATTAA AGAGCAAAAAC TAASATTAA AGAGCAAAAAA AGAGCAAAAAAA AGAGCAAAAAAAA
2701	Argalagiu Lysbysiip Magazia Totalagaria Actorcanta Tgatagaria
	TYTLYSGIU AIGLYSSIA TACCATTCGA
2761	GINALAASP THIASHITE MAANACAA
2823	GINALASP THRASHITE AIGHESTER GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA GUALATYR LeuProGlu LeuSerVallle ProGlyVal AsnAlaAla IlePheGluGlu GLUALATYR LEUProGlu LeuSerVallle ProGLYVAL CCAGAAATGT CATTAAAAAT
288	TTAGAAGGGC GTATTTTCAC TGCATTCTCC CTATATGATG CGAGAMITO
294	1 GGTGATTTTA ATAATGGCTT ATCCTGCTGG AACGTGAAAG GGCATGTAOAT
300	ACCOMMOGO CONTROLL CONTROLL CONTROLL ValserGlnGlu

Fig. 15D

3061	GTTCGTGTCT GTCCGGGTCG TGGCTATATC (ValArgVal CysProGly ArgGlyTyrIle)	
3121	GGAGAAGGTT GCGTAACCAT TCATGAGATC	GAGAACAATA CAGACGAACT CAMCTELE GluAsnAsn ThrAspGlu LeuLysPheSer
3181	AACTGTGTAG AAGAGGAAGT ATATCCAAAC	AACACGGTAA CGTGTAATGA TTAIMSTOA AsnThrVal ThrCysAsn AspTyrThrAla
3241	ACTCAAGAAG AATATGAGGG TACGTACACT	TCTCGTAATC GAGGATATON STATES SERARGASN ARGGLYTYR ASPGLYALATYR
3301	GAAAGCAATT CTTCTGTACC AGCTGATTAT	GCATCAGCCT ATGAAGAAAA AGGAAAA AGGAAAA AGGAAAAA AGGAAAAAA
3361	GATGGACGAA GAGACAATCC TTGTGAATCT	AACAGAGGAT AIGGGGATTA SANARGGLY TYRGLYASP TYRThrProLeu
3421	CCAGCTGGCT ATGTGACAAA AGAATTAGAG	TACTTCCCAG AAACCGATAA GUALTIPILE TyrPhePro GluThrAsp LysValTrpIle
3481	GAGATCGGAG AAACGGAAGG AACATTCATC GlulleGly GluThrGlu GlyThrPheIle	GTGGACAGCG TGGAATTACT TCTTATGGAG ValAspSer ValGluLeu LeuLeuMetGlu
3541	GAATAAG Glu	

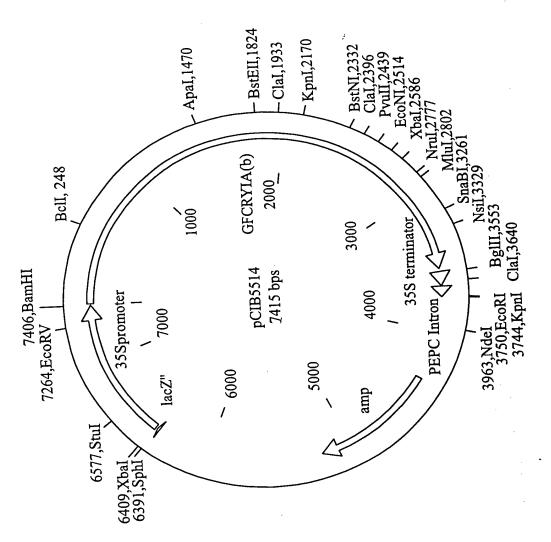
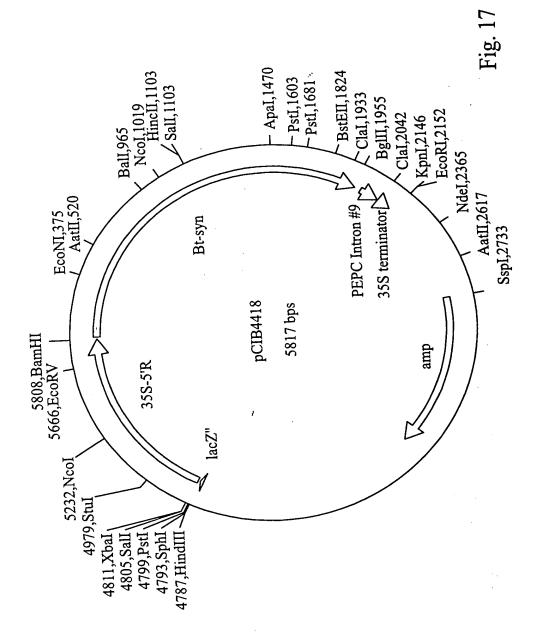
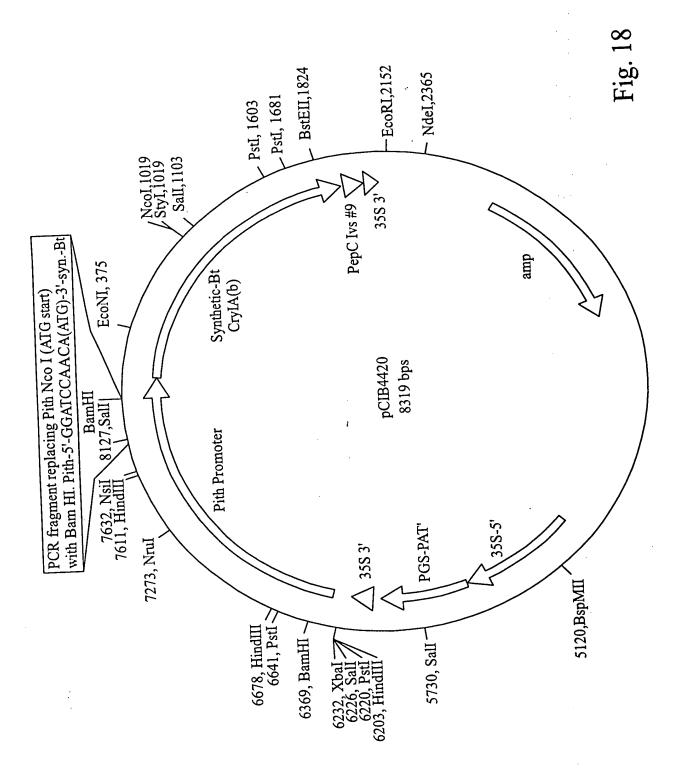


Fig. 16





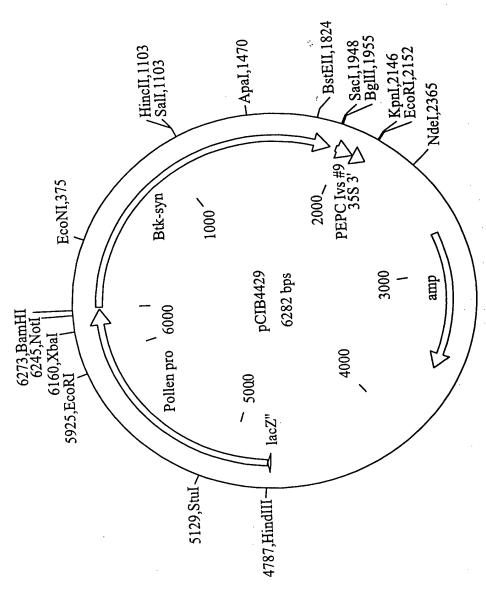
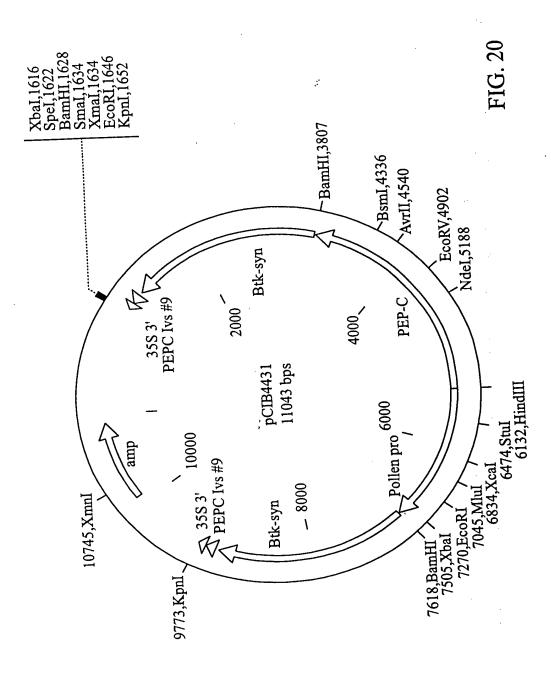


FIG. 19



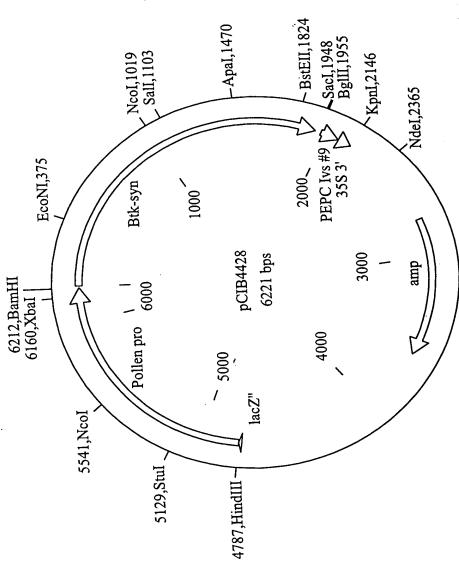


FIG. 21

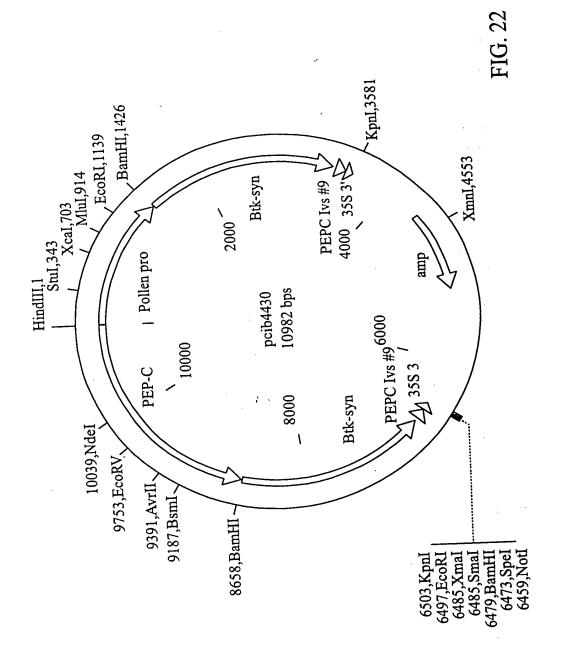


Fig. 23A

CrylA(b) Protein Levels in Transgenic Maize

ELISA Bt Values of Field Plants:

INBRED X PARENT AE	BRU PLANT Number	ng Bt/mg protein
2ND01X171-4A 5N984X171-4A 5N984X171-13 5N984X171-15 5N984X171-15 5N984X171-14A 5N984X171-14A 5N984X176-11 5N984X176-11 5N984X176-11 5N984X176-11 5N984X171-4B 5N984X171-4B 5N984X171-4B 5NA56X171-16ABX 5NA89X176-11 5NA89X176-11 5NA89X176-11 6F010X171-4 6F010X171-4	1646 857 870 969 1468 1470 1502 1529 1667 1671 1673 1675 1679 1942 1946 1101 1622 1630 1635 825 832	29 1705 1760 22 17 28 180 1500 408 1270 1522 943 967 15 16 30 959 1172 1100 103 1298

- -Bt levels are in ng crylA(b)/mg total protein.
- -Data are from progeny of the described maize transformants expressing the crylA(b) protein.
- -ELISA analysis of transgenic plant material was carried out using standard procedures as described elsewhere.

Bioassay of European corn borer, Ostrinia nubilalis, and sugarcane borer, Diatraea saccharalis Fig. 23B

Bioass	ay or Europe	Bloassay of European com bolor,				
					Percent Mortality	Nortality
ī	() ()	Cross	Plant No.	Bt Gene	Ostrinia	Diatraea
Plasmid	FIOIIIOIE				100	100
-CID4434		5N984 X 176-8B	21	+	<u> </u>	0
pCi04450) Ī		22 40	· +	100	100
nCIB4431	PEPC	5N984 X 176-11	95	+ '	100	100
			0 8 0	+	100	100
pCIB4418	358	5N984 X 171-14A	45 64	٠+	100	90
			- 89	+	. 100	001
DCIB4431	PEPC	2N217AF X 176-8B	← α	. +	100	100
·-			0 4	+	100	100
2CIBAA18	358	2N217AF X 171-15		٠ -	10	0 8
			က ထ ထ ထ	+ +	06	100

Fig. 23C

CrylA(b) Protein Levels in Transgenic Maize

Greenhouse plants

35S LINE 6F010 x 171-4A 5N984 x 171-14A 6F010 x 171-16AB 5N984 x 171-13 5NA89 x 171-13 5N984 x 171-18 6N615 x 171-16AB	LEAF -409 + 288 256 + 159 240 + 174 201 + 94 37 + 7 7.7 + 3 7.5 + 3	PITH NT 191 221 NT 150 NT 0	ROOT NT 198 271 NT 0 NT 0	POLLEN NT 30 NT NT NT NT NT
PEPC LINE 6N615 x 176-11 6F010 x 176-10 5N984 x 176-11	1126 + 419 774 + 159 719 + 128	41 NT 16	19 NT 20	NT 130 186

-Bt levels are in ng crylA(b)/mg total protein.

Data are from progeny of the described maize transformants expressing the crylA(b) protein.

ELISA analysis of transgenic plant material was carried out using standard procedures as described elsewhere.

Bioassay of European corn borer, Ostrinia nubilalis, on Pith:SynBt maize Fig. 23D

Percent Mortality	90 80 90 70 75 85	70 65 85 95	0 0
Plant No.	1 5 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3 7 17	7 2 8
Event	JS21A-Top	JS22D-Mid	Control
Promoter	Pith	Pith	
Plasmid	pCIB4433	pCIB4433	

Fig. 23E

EXPRESSION OF THE CRYIA(b) GENE IN TRANSGENIC MAIZE USING THE PITH-PREFERRED PROMOTER

Leaf samples from small plantlets transformed with pClB4433 using procedures described elsewhere were analyzed for the presence of the crylA(b) protein using ELISA. All plants expressing crylA(b) were found to be insecticidal in the standard European corn borer bioassay.

Note that the pith-preferred promoter has a low, but detectable level of expression in leaf tissue of maize. Detection of CrylA(b) protein is consistent with this pattern of expression.

PLANT NUMBER	ng crylA(b)/mg protein
JS21A-1 TOP JS21A-2 TOP JS21A-3 TOP JS21A-11 TOP JS21A-12 TOP JS21A-14 TOP JS21A-19 TOP JS21A-24 TOP JS21A-28 TOP JS22D-3 MID JS22D-11 MID JS22D-11 MID JS22D-17 MID	169 0 113 127 112 97 118 82 0 154 2946 5590 215 3004

Fig. 24A

1 GAATTCGGATCCATTAAAGAAGTCTTTGAACAGATTCTAGAGATCTAGTTTAATGAGCTC 61 CCAAAAGTCTTGAAAAAATTCAGCGGGGGAGCCATTAGGGCAGGGGTACTGTTATGTTTT 120 121 AAAGAGAACACCACTTTCTTCATCTCTTCTTAAAGAGAAATGTTTTGTAAGAAGGATCCTG 180 181 TCCTCCTCATCCAACCTTTTCATCGGCAAATTTTTCATAGAGGCAAGAGAG 240 GGGCCAAAAAGATCCATGTAAATGGAAGTGGCCACCTGGTTGATACCTCCCTC	
1261 CAGCCAGCCATGTGGCACTCCTACGTATACTACGTGAGGTGAGATTCACTCAC	
1321 GGGACCGAGATATTTTACTGCTGTGTGTGTGAGAGATATAAAGGATTTTTATTCGCATGCA 1440	
1441 TGTTTCATTATCATATATATATATAACACATATTAAATGATTCTTCGTTCCAATT 1500 -226 -285	
1501 TATAATTCATTTGACTTTTTTATCCACCGATGCTCGTTTTATTAAAAAAAA	
1561 TATTGTTACTTTTTGTTGTAATATTGTTTAGCA <u>TATAAT</u> AAACTTTGATACTAGTATGTT 1620 -106	
1621 TCCGAGCAAAAAAAATATTAATTTAGATTACGAGCCCATTAATTA	
1681 ACAAGCGAAGCAAAGCAAGCAAGCTAATGTTGCCCCTGCTGTGCATGCA	
1741 CTTGCTATAAACGAGGCAGCTAGACGCGACTCGACTCATCAGCCTCATCAACCTCGACTCATCAGCCTCATCAACCTCGACTCATCAGCCTCATCAACCTCGACTCATCAGCCTCATCAACCTCGACTCATCAACCTCGACTCATCAACCTCGACTCATCAACCTCGACTCATCAACCTCGACTCATCAACCTCGACTCATCAACCTCGACTCATCAACCTCGACTCATCAACCTCGACTCATCAACCTCGACTCATCAACCTCGACTCATCAACCTCGACTCATCAACCTCGACTCAACCTCAACCTCGACTCAACCTCGACTCAACCTCGACTCAACCTCGACTCAACCTCGACTCAACCTCGACTCAACCTCGACTCAACCTCGACTCAACCTCGACTCAACCTCGACTCAACCTCGACTCAACACAACA))

Fig. 24B

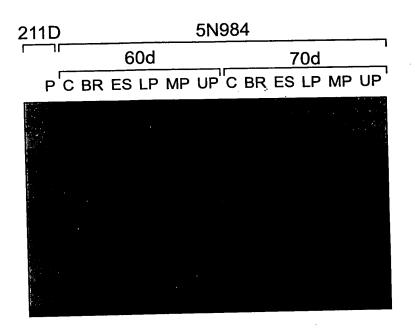
1861 C +126	CTCC S	TCC S	CTC(S	CTC S	GCT L	GTC S	CTC S	CGG A	CG'	TT(L	GCA Q	GG(A	CAC	GCT A	rca Q	GT(S	CGC P	CGC	CG	CT(L	GCT L	CC'.	rga R	19 +1	20 95
1921 G +196	GCG(R	GAT(M	GTC S	GTC S	GAC T	CGC A	AA: T	CAC P	CG.	AG R	ACG R	GA R	GG'	ľA(Y	CGA D	CG(A	CGG) + CC() +	41 GTC J	GT V	CG'I	CA T	CTA T	19 +2	80 55
1981 (+256	CCAC(CAC T	CAC T		TAG R	AGC A	TG(A	CGC A	CG	GC A	TG(A	CTG V	TC	AC T	GGI . V	TC P	CCG F	SCC(GCC A	CC P	GC(P	CGC Q	AGG A	20 +3	40 15
2041 (+316	G	R	R	R	ĸ		Π	` '	2	U		-	•		GC <i>I</i> H									+3	100 375
2101	CGGT	GTC	:GG <i>I</i>	ACA(T	CCA!	GGO A	H	١.	L	T.T	11			_											
2161 2221	GCTA	\GA'J	L'CA	rcG	GIU	CAG	T	A	F		I .	P	Y]	[T	Α	G	D]	Ρ.	ט	Ъ		
2281	7 7	י ק	ľ	А	E	A.	ப	1/	1.1				_		-										
2341	GGG(.7	D	C	S	D)	Ρ.	1			ט	0	-		_		~								
2401	7\ '	T	Δ	S	(-)	Т	1	1,1	ν	,	LI	•			_								GCCG P CTTG L		
24612521		Т	C	('	Ρ	V	V	u	Τ.	J	U	_	_												
2521 2581	A	E	M	K	Ľ	A	G	٧	•	•			~ 3 .		mm	លាយ។	n C m	ատվ	ירויי	արարո	րդի	AC	rgaci	A :	2640 2700
2641	GGT	'CT'	TAT T	AGT V	GCC P	TGA D	L	P	CG.	Y	V	A	Ĩ	Ā	Н	S	\mathbf{L}	, V	J	S	Ε	Α	K		2760
	3.7	N	N		۲.																				2820
				GAI	'GAA	.GG <i>I</i>	\GA'	TC <i>P</i>	יכר	ממי	GGO	ርጥጥ	'CA	GA	AGO		TC								2880
288	E l TG	D TAT	ATA	M TAC OGAC	ATO	GA(- CGA AGA	CGT CCI	'AA'	CT SAC	'CA' 'GA'	TTC CGP	CA	GC 'AA	CC(CAT CTA	GCZ .GC'	ATA TAG	TAT GG('GG GCG	AG TA	GCT CGT	TCAF TGCF	AT AG	2940 3000
300	1 IC 1 GT V	GAG	CGI V	[GA]	ACG(G	GAG' V	ΓGA	CAC	GG'I G	CC P	TC	GCG	GC <i>P</i> A	AA	.CG' V	rga N	AC(CCA P	CGI R	AGI V	GG E	AGT	CACT	rc	3060

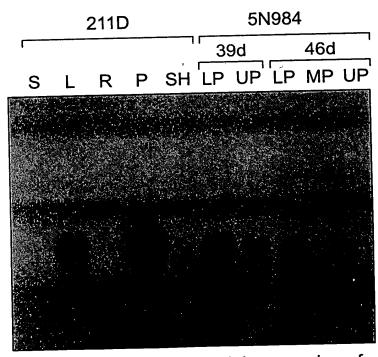
Fig. 24C

3061 ATCCAGGAGGTTAAGAAGGTGACTAACAAGCCCGTTGCTGTTGGCTTCGGCATATCCAAG 3120 I O E V K K V T N K P V A V G F G I S K
3121 CCCGAGCACGTGAAGCAGGTACGTACGTAGCTGACCAAAAAAAA
P E H V K 3181 TTTGACAAGCCGGCTACTAGCTAACAGTGATCAGTGACACACAC
3241 TGCGCAGTGGGGCGCTGACGGGGTGATCATCGGCAGCGCCATGGTGAGGCAGCTGGGCGA 3300 A Q W G A D G V I I G S A M V R Q L G E
3301 AGCGGCTTCTCCCAAGCAAGGCCTGAGGAGGCTGGAGGAGTATGCCAGGGGCATGAAGAA 3360
+++ 3361 CGCGCTGCCATGAGTCAAAAGTAAAACGTACAGAGACACTTGATAATATCTATC
A L P 3421 ATCATCTCGGAGAAGACGACCGACCAATAAAAATAAGCCAAGTGGAAGTGAAGCTTAGCT 3480
3421 ATCATCTCGCMANAGEMENT 3481 GTATATACACCGTACGTCGTCGTCGTCGTCGGATCGATCTCGGCCGGC
3661 CGAAGAAGCTGGCTAGCTAGCCGTCTCGATCGTATATGTACTGATTAATCTGCAGATTGA 3720
3721 ATAAAAACTACAGTACGCATATGATGCGTACGTTGTGTATAGITITGTGTCACTACTCTGTTAAATG 3781 GCTCCTCATCACCTGCCTGATCTGCCCATCGATCTCTCTGTACTCCTGTTAAATG 3841 CCTTCTTTGACAGACACCACCACCAGCAGCAGCAGCTGAGCACTCTGCACGCCGCCGCTTTAA 3900 3841 CCTTCTTTGACAGACACACCACCACCAGCAGCAGCAGCTGAGCACCAAATCTGGAGCACTGGG 3961 GACATGTAAGATATTTTAAGAGGTATAAGATACCAAGGAGCACAAAATCTGGAGCACTGGG 3961 ATATTGCAAAGACAAAAAAAAAAAAAATTTAAGGTCCCACCAAAGTAGAGATAGTAAAGA 4021 GGTGGATGGATTAAAATTATCTCATGATTTTTGGATCTCTCAAATAGATCGATATGGTA 4081 TTCAGATCTATGTTGTATAGCCTTTTCATTAGCTTTCTGAAAAAAAA
Entire sequence of the maize TrpA gene, with introns

Entire sequence of the maize TrpA gene, with introns and exons, transcription and translation strats, start and stop of cDNA.

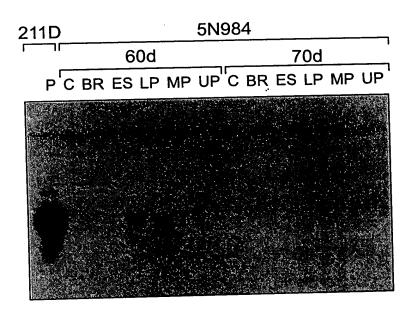
\$ = start and end of cDNA; +1 = transcription start; 73****** = primer extension primer; ▼ = start of translation; +++ = stop codon; = CCAAT Box, TATAA Box, poly A addition site. # above underlined sequences are PCR primers.

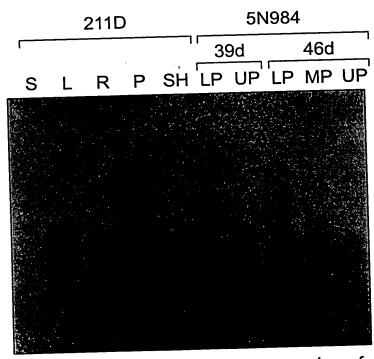




Northern blot showing differential expression of TrpA gene in maize tissues. 2 hour exposure against film at -80C with Dupont Cronex intensifying screens.

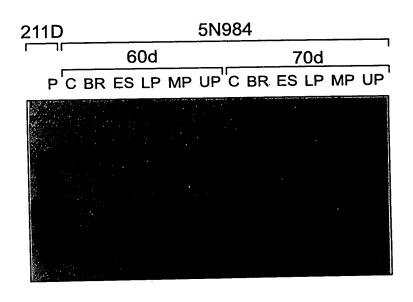
Fig. 25A

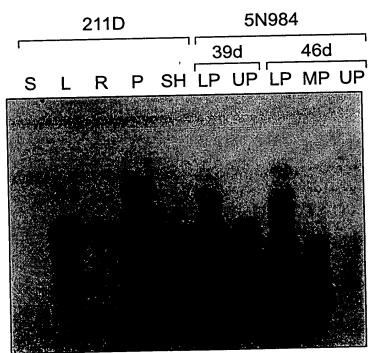




Northern blot showing differential expression of TrpA gene in maize tissues. 4 hour exposure against film at -80C with Dupont Cronex intensifying screens.

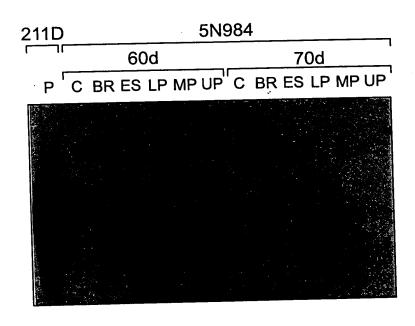
Fig. 25B

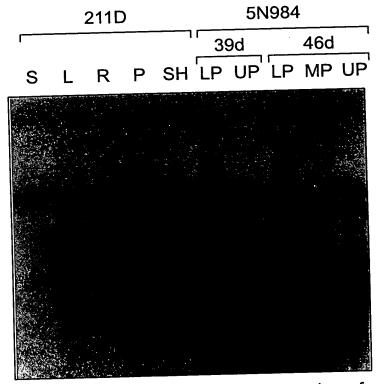




Northern blot showing differential expression of TrpA gene in maize tissues. 18 hour exposure against film at -80C with Dupont Cronex intensifying screens.

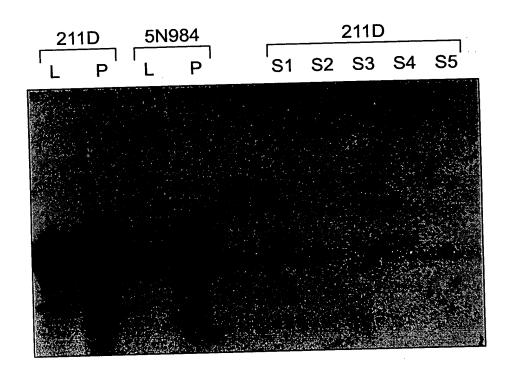
Fig. 25C





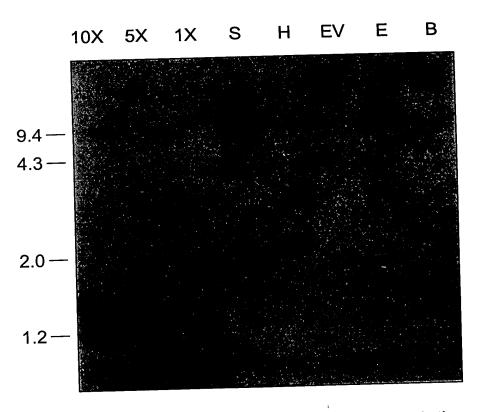
Northern blot showing differential expression of TrpA gene in maize tissues. 48 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 25D



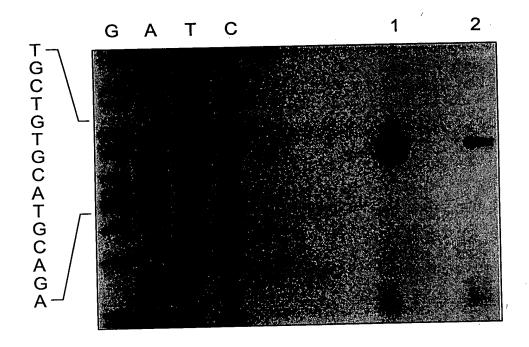
Northern blot showing maize TrpA gene expression in Funk lines 211D and 5N984 leaf and pith and the absense of expression in 211D seed total RNA. 65 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 26



Genomic southern of Funk line 211D probed with the TrpA cDNA 8-2. B = BamHI, E = EcoRI, EV = EcoRV, H = HindIII and S = SacI. 120 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 27

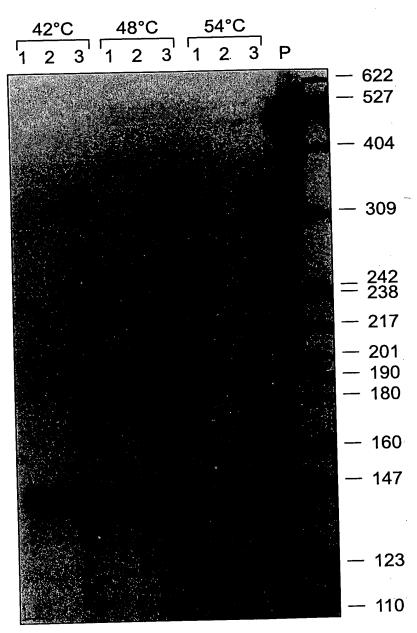


Primer extension showing the transcription start of TrpA gene and sequencing ladder.

1 hour exposure against film at -80C with Dupont Cronex

intensifying screens.

Fig. 28A



RNase protection of region from +2 bp to +387 bp with three annealing temperatures.

16 hour exposure against film at -80C with Dupont Cronex intensifying screens.

Fig. 28B

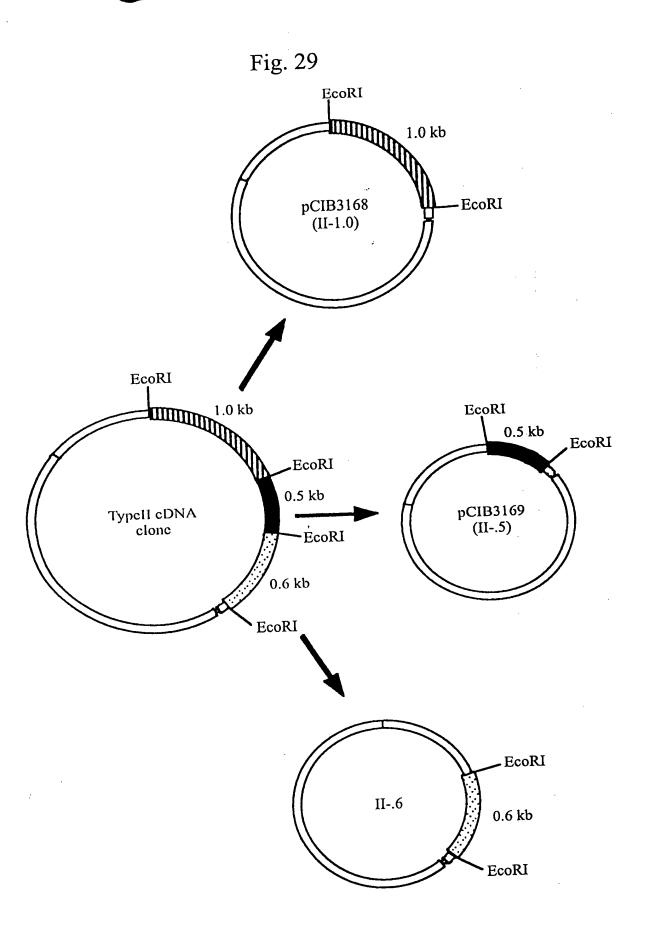


Fig. 30B

969 CTG GAT AGA GAA GAG CAC CTT TAC ACA GCA TTC CAG TAT TTC GAC AAG GAC AAC AGC 323 Leu Asp Arg Glu Glu His Leu Tyr Thr Ala Phe Gln Tyr Phe Asp Lys Asp Asn Ser 1026 GGG TAC ATT ACT AAA GAA GAG CTT GAG CAC GCC TTG AAG GAG CAA GGG TTG TAT GAC 342 Gly Tyr Ile Thr Lys Glu Glu Leu Glu His Ala Leu Lys Glu Gln Gly Leu Tyr Asp

1083 GCC GAT AAA ATC AAA GAC ATC ATC TCC GAT GCC GAC TCT GAC AAT GAT GGA AGG ATA 361▶Ala Asp Lys Ile Lys Asp Ile Ile Ser Asp Ala Asp Ser Asp Asn Asp Gly Arg Ile

1140 GAT TAT TCA GAG TTT GTG GCG ATG ATG AGG AAA GGG ACG GCT GGT GCC GAG CCA ATG 380▶Asp Tyr Ser Glu Phe Val Ala Met Met Arg Lys Gly Thr Ala Gly Ala Glu Pro Met

Fig. 30A

Maize Pollen CDPK cDNA sequence sequence contained in clones pCIB3168 and pCIB3169

1 TG CAG ATC ATG CAC CAC CTC TCC GGC CAG CCC AAC GTG GTG GGC CTC CGC GGC GCG 1▶Gln Ile Met His His Leu Ser Gly Gln Pro Asn Val Val Gly Leu Arg Gly Ala

57 TAC GAG GAC AAG CAG AGC GTG CAC CTC GTC ATG GAG CTG TGC GCG GGC GGG GAG CTC 19▶Tyr Glu Asp Lys Gln Ser Val His Leu Val Met Glu Leu Cys Ala Gly Gly Glu Leu

114 TTC GAC CGC ATC ATC GCC CGG GGC CAG TAC ACG GAG CGC GGC GCC GCG GAG CTG CTG 38▶Phe Asp Arg Ile Ile Ala Arg Gly Gln Tyr Thr Glu Arg Gly Ala Ala Glu Leu Leu

171 CGC GCC ATC GTG CAG ATC GTG CAC ACC TGC CAC TCC ATG GGG GTG ATG CAC CGG GAC 57▶Arg Ala Ile Val Gln Ile Val His Thr Cys His Ser Met Gly Val Met His Arg Asp

228 ATC AAG CCC GAG AAC TTC CTG CTC AGC AAG GAC GAG GAC GCG CCG CTC AAG GCC 76▶Ile Lys Pro Glu Asn Phe Leu Leu Leu Ser Lys Asp Glu Asp Ala Pro Leu Lys Ala

285 ACC GAC TTC GGC CTC TCC GTC TTC TTC AAG GAG GGC GAG CTG CTC AGG GAC ATC GTC 95▶Thr Asp Phe Gly Leu Ser Val Phe Phe Lys Glu Gly Glu Leu Leu Arg Asp Ile Val

342 GGC AGC GCC TAC TAC ATC GCG CCC GAG GTG CTC AAG AGG AAG TAC GGC CCG GAG GCC 114▶Gly Ser Ala Tyr Tyr Ile Ala Pro Glu Val Leu Lys Arg Lys Tyr Gly Pro Glu Ala

399 GAC ATC TGG AGC GTC GGC GTC ATG CTC TAC ATC TTC CTC GCC GGC GTG CCT CCC TTC 133▶Asp Ile Trp Ser Val Gly Val Met Leu Tyr Ile Phe Leu Ala Gly Val Pro Phe

456 TGG GCA GAG AAC GAG AAC GGC ATC TTC ACC GCC ATC CTG CGA GGG CAG CTT GAC CTC 152 Trp Ala Glu Asn Glu Asn Gly Ile Phe Thr Ala Ile Leu Arg Gly Gln Leu Asp Leu

513 TCC AGC GAG CCA TGG CCA CAC ATC TCG CCG GGA GCC AAG GAT CTC GTC AAG AAG ATG 171▶Ser Ser Glu Pro Trp Pro His Ile Ser Pro Gly Ala Lys Asp Leu Val Lys Lys Met

570 CTC AAC ATC AAC CCC AAG GAG CGG CTC ACG GCG TTC CAG GTC CTC AAT CAC CCA TGG 190▶Leu Asn Ile Asn Pro Lys Glu Arg Leu Thr Ala Phe Gln Val Leu Asn His Pro Trp

627 ATC AAA GAA GAC GGA GAC GCG CCT GAC ACG CCG CTT GAC AAC GTT GTT CTC GAC AGG 209▶Ile Lys Glu Asp Gly Asp Ala Pro Asp Thr Pro Leu Asp Asn Val Val Leu Asp Arg

684 CTC AAG CAG TTC AGG GCC ATG AAC CAG TTC AAG AAA GCA GCA TTG AGG ATC ATA GCT

228▶Leu Lys Gln Phe Arg Ala Met Asn Gln Phe Lys Lys Ala Ala Leu Arg Ile Ile Ala

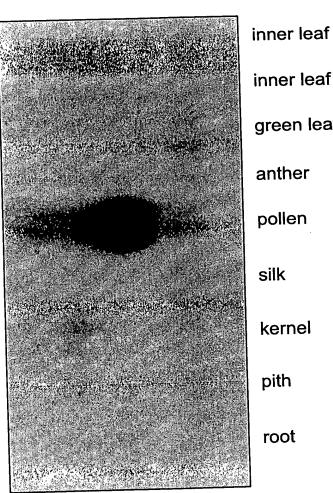
741 GGG TGC CTA TCC GAA GAG GAG ATC ACA GGG CTG AAG GAG ATG TTC AAG AAC ATT GAC 247▶Gly Cys Leu Ser Glu Glu Glu Ile Thr Gly Leu Lys Glu Met Phe Lys Asn Ile Asp

798 AAG GAT AAC AGC GGG ACC ATT ACC CTC GAC GAG CTC AAA CAC GGG TTG GCA AAG CAC 266 Lys Asp Asn Ser Gly Thr Ile Thr Leu Asp Glu Leu Lys His Gly Leu Ala Lys His

855 GGG CCC AAG CTG TCA GAC AGC GAA ATG GAG AAA CTA ATG GAA GCA GCT GAC 285▶Gly Pro Lys Leu Ser Asp Ser Glu Met Glu Lys Leu Met Glu Ala Ala Asp Ala Asp

EcoRI

912 GGC AAC GGG TTA ATT GAC TAC GAC GAA TTC GTC ACC GCA ACA GTG CAT ATG AAC AAA 304▶Gly Asn Gly Leu Ile Asp Tyr Asp Glu Phe Val Thr Ala Thr Val His Met Asn Lys



inner leaf sheath inner leaf whorl green leaf

Fig. 31

Fig. 32

Lipman-Pearson Gap Penalty: 2 Seq1	• Gan benguu	cimilarity	Gap Number	Gap Length	Consensus Length
pol CDPK ptn 1>551	1>528	36.5	4	4	297

pol CDPK ptn YSMGKELGRGQFGVTHLCTHRTSGEKLACKTIAKRKLAAREDVDDVRREVQIMHHLSGQPNVVGLRGAYE 162 Y: .ELG:G.F:V.: C..:TS.:. A K.I..:KL:AR:: :: RE.:I : L. :PN:V L::: . rat pk2 ptn YQLFEELGKGAFSVVRRCVKKTSTQEYAAKIINTKKLSARDH-QKLEREARICRLLK-HPNIVRLHDSIS 81

pol CDPK ptn DKQSVHLVMELCAGGELFDRIIARGQYTERGAAELLRAIVQIVHTCHSMGVMHRDIKPENFLLLSKDEDA 232 : .LV.:.:GGELF: I:AR. Y:E:A:::.I:: V: H:::HRD:KPEN:LL SK .:A : .LV.:.:GGELF: DIVAREYYSEADASHCIHQILESVNHIHQHDIVHRDLKPENLLLASKCKGA 151

pol CDPK ptn KQFRAMNQFKKAALRII 387 ::F.A..::K A L .: RKFNARRKLKGAILTTM 308

Fig. 33

Gap Penalty: Seq1 pol CDPK ptn	Seq2 humcama ptn	t alty: 12 Similarity Index 40.3		Gap Length 2	Consensus Length 142	
1>551	1>150	10.0				
pol CDPK ptn humcama ptn	LSEEEITGLKEMFKNIDKDNS L:EE:I:.:KE F. :DKD LTEEQIAEFKEAFSLFDKDGD	GTIT EL : G	.: :::E::.	:::DADGN	G ID: Fr:T	
pol CDPK ptn humcama ptn	HMNKL-DREEHLYTAFQYFDH : M:. D.EE:: .AF: FDH RKMKDTDSEEEIREAFRVKDH	KD :GYT: .EL H.:.	; G:	:::1.:AD	D.DG:::I.Erv.	
pol CDPK ptn	мм 530 мм мм 146					

Fig. 34

Lipman-Pearson E Gap Penalty: 2; Seq1 pol CDPK ptn	Gap Length Pe	nalty: 12 Similarity ptn Index		Gap Length	Consensus Length		
1>551	1>509	62.4	,1	1	464		
pol CDPK ptn soybean CDPK ptn	VLGRPMEDVRATYSMG :. ::: .: VLPQRTQNIREVYEVG	KELGRGQFGVTHLCTH :. : . : RKLGQGQFGTTFECTF	RTSGEKLAC : . : RRASGGKFAC	KTIAKRKLA : : CKSIPKRKLL	AREDVDDVRREVQIM : : : : CKEDYEDVWREIQIM	HHLSG . HHLSE	150 91
pol CDPK ptn soybean CDPK ptn	QPNVVGLRGAYEDKQS :: : : . : HANVVRIEGTYEDSTA	VHLVMELCAGGELFDF VHLVMELCEGGELFDF	RIIARGQYTE :.: : : RIVQKGHYSE	ERGAAELLRA ::: ERQAARLIKT	IVQIVHTCHSMGVMH :: :: : IVEVVEACHSLGVMH	RDIKP : RDLKP	220 161
pol CDPK ptn soybean CDPK ptn	ENFLLLSKDEDAPLKA : : ENFLFDTIDEDAKLKA			• • • • • • • •			290 231
pol CDPK ptn soybean CDPK	PPFWAENENGIFTAII	LRGQLDLSSEPWPHIS : : LLGKLDFHSEPWPSIS	PGAKDLVKKI : :: DSAKDLIRK	MLNINPKERI : . MLDQNPKTRI	TAFQVLNHPWIKEDO : . : . LTAHEVLRHPWIVDDN	DAPDT . IIAPDK	360 301
pol CDPK ptn soybean CDPK ptn	PLDNVVLDRLKQFRAM	MNQFKKAALRIIAGCL :: : . MNKLKKMALRVIAERL	SEEEITGLK SEEEIGGLK	EMFKNIDKDI : . ELFKMIDTDI	NSGTITLDELKHGLAH : : NSGTITFDELKDGLKH	(HGPKL : :. ≀VGSEL	430 371
pol CDPK ptn soybean CDPK ptn	SDSEMEKLMEAADAD : : : MESEIKDLMDAADID	GNGLIDYDEFVTATVH : : :: KSGTIDYGEFIAATVH	MNKLDREEH : : : LNKLEREEN	LYTAFQYFD : LVSAFSYFD	KDNSGYITKEELEHA . : ::: KDGSGYITLDEIQQA	LKEQGL : CKDFGL	500 441
pol CDPK ptn soybean CDPK ptn	1 1 1 1 1 1 1	DNDGRIDYSEFVAMMR : : DNDGQIDYGEFAAMMR	11.:1	.::1			

Fig. 35A

pol CDPK gene Map (1 > 4165)

Site and Sequence

6 of 198 enzymes (Filtered) Enzymes: Circular, Certain Sites Only, Standard Genetic Code Settings: TTAGTAACACCTCTCCAATCGCTTGGGTTGGCACATTCTTAGCTTTTATCACATTTTAAGAAATAGAGTTCACCACCTTC AAAATATGCCTATACAATGAATGATGCTTGGATGCAATATAGCTAGATTCAACTAGCTATATATGGTCAATAGAACCCTG TGAGCACCTCACAAACACGACTTCAATTTTGAGACCCTAAGCGAGTAAATGGTTAAAGTCCTCTTATTATTAGTCTTAGG CTAGGGTATCTCAAAGGCCTAGTCACAACAATTCTCAACAGTATTTAATTTTATACATGTATGAACAGTGTAGGAATTTG 400 AGTGCCCAACCCAAGAGTGGGAGGTGTAAATTGGGTAGCTAAACTTAAATAGGGCTCTTCTTATTTAGGTTTATCTAGTC 480 TCTACTTAGACTAATTCAGAAAGAATTTTACAACCTATGGTTAATCATATCTCTAGTCTAAGCAAATTTAGGAAAGTTAA 560 TGTGGTGGTATATCCCAATGATATTAGATGCCAGAATATAGGGGGGAAATCGATGTATACCATCTCTACCAGGATACCTG 720 TGCGGACTGTGCAACTGACACATGGACCATGGTGTCTTCTTAGATTTGGTTATTAGCTAATTGCGCTACAACTTGTTCAA 800 GGCTAGACCAAATTAAAAAAACTAATATTAAACATAAAAAGTTAGGCAAACTATAGTAAATTATGCAGCGATCCAACAACA 880 AGCCATGTCTCGTGGGTCATGAGCCACGCGTCGGCCATACACCCACATGATGTTTCCATACGGATGGTCCTTATGCAATT TTGTCTGCAAAACACAAGCCTTAATACAGCCACGCGACAATCATGGAAGTGGTCGTTTTAGGTCCTCATCATGAAGTTCA GGGAAAACGCATCAAATGTAATGCAGAGAAATGGTATTTCTTCTCTTGTAAATCAGGGAGAGGAGTACCATCAGTACAGA TTCAGAATCAGAATTCAGTCTTCCAACGACAATAATCGCAGCATCTTGTAAAAATTTGCAGAAACTTCTGTTTGACTTGT AGCCCTGACCTTTGCAAATATTTGAAGTTGTGCCTGCTGACACAACTTCAATCTGGAAGTGCTGTTGATCAGTTTTGCCA

Fig. 35B

CDPK gene Map (1 > 4165) Site and Sequence	
Xba I	
AAATCTAGAAACCTTTTTTTTCCTCCCGATACGCCCCTCCATCTCTCGCCGTTCATGTCCGTGGCTGGC	1440
	1770
I _{mRNA} start J	
	Δ
GGGAGCAGGCGGCCGCACTCGTTCCCCGCCGCAGCCATGGGCCAGTGCTGCTCCAAGGGCGCCGGAGAGGCCCCGCC	152
EXON 1	_
CGAGGCGCCAAACGGCAGGCGCCAAGCCGCGGGCGTCCGCGAACAACGCCGACGGACAACGGGCGTCGTCCTCGTCCG	ር - 160
	_
— EXON 1———	
GTGGCTGCTGCCGCTGCTGCCGGTGGTGGTGGCGGCGCGCACGACGAAGCCGGCCTCACCCACC	iG
GTGGCTGCTGCTGCTGCTGCCGGTGGTGGTGGTGGTGGTG	<u> </u>
EXON 1	=
	-c
CAGCTCCGGCAGCAAACCGGCGGCGGCCGTGGGCACGGTGCTGGGCCGGCC	그 17
EXON 1	
Ava I	
ATGGGCAAGGAGCTCGGGCGCGGCAGTTCGGCGTGACGCACCTGTGCACGCAC	TG 18
EXON 1	
CAAGACGATCGCGAAGCGGAAGCTGGCGGCCAGGGAGGACGTGGACGACGTGCGGCGGGAGGTGCAGATCATGCACCA	cç
CAAGACGATCGCGAAGCTGGCGGCACC	<u></u> 19
EXON 1	
	rgc
TCTCCGGCCAGCCCAACGTGGTGGGCCTCCGCGGCGCGTACGAGGACAAGCAGAGCGTGCACCTCGTCATGGAGCTG	20
SVOVI	
EXON 1	
Ava I	
GCGGGCGGGGGGCTCTTCGACCGCATCATCGCCCGGGGCCAGTACACGGAGCGCGCGC	CAT 20
EXON 1	

Fig. 35C

CDPK gene Map (1 > 4165)	Site and Sequence
	Ava I
GTGCAGATCGTGCACACCTGCCACTCC	ATGGGGGTGATGCACCGGGACATCAAGCCCGAGAACTTCCTGCTGCTCAGCA
	EXON 1
	CGACTTCGGCCTCTCCGTCTTCTTCAAGGAGGGCGAGCTGCTCAGGGACATC
GGACGAGGACGCGCCGCTCAAGGCCAC	22
	EXON 1
Ava	.1
TCGGCAGCGCCTACTACATCGCGCCCC	AGGTGCTCAAGAGGAAGTACGGCCCGGAGGCCGACATCTGGAGCGTCGGCGT 2
	EXON 1
	Bam H I
ATGCTCTACATCTTCCTCGCCGGCGT	GCCTCCCTTCTGGGCAGGTCGGATCCGTCCGTGTTCGTCCTAGACGATATACA
	INTRON 1
EXON 1-	
BAACCCGACGATGGATTTGCTTCTCAG	CCCTGTTCTTGCATCACCAGAGAACGAGAACGGCATCTTCACCGCCATCCTGC
INTRON	1——EXON 2———
	CATGGCCACACATCTCGCCGGGAGCCAAGGATCTCGTCAAGAAGATGCTCAAC
GAGGGCAGCTTGACCTCTCCAGCGAGC	CATGGCCACATCTCGCCGGGACCO
	EXON 2
ATCAACCCCAAGGAGCGGCTCACGGCC	STICCAGGICCICAGIAAGIACCCAGAICGIIGCIGICATACACICATAIGAAI
EXON 2 —	INTRON 2
	202024040404040404040404040404040404040
TGTATCGTTCATGAGCAACGATCGAG	CGGATTTGGTGAACTTGTAGATCACCCATGGATCAAAGAAGACGGAGACGCGCC
INTRON	EXON 3
T0404C0CCCCCTTC4C4ACCTTCTTC	TCGACAGGCTCAAGCAGTTCAGGGCCATGAACCAGTTCAAGAAAGCAGCATTGA
IGACACGCCGC I IGACAACGT IGTIC	TEGRACAGETERAGON
	EVONO
	EXON 3

Fig. 35D

CDPK gene Map (1 > 4165) Site and Sequence	
TO THE TOTAL AND CONTRACT OF A CANCELL CONTR	2880
INTRON 3	
•	
TGCTCTTGATGACATAATGTTAGATCATAGCTGGGTGCCTATCCGAAGAGGAGATCACAGGGCTGAAGGAGATGTTCAA	2960
INTRON 3—EXON 4	
AACATTGACAAGGATAACAGCGGGACCATTACCCTCGACGAGCTCAAACACGGGTTGGCAAAGCACGGGCCCAAGCTGT	304
AACATTGACAAGGATAACAGGGGAACA	304
EXON 4———	
CAGACAGCGAAATGGAGAAACTAATGGAAGCAGTGAGTTTTCAGAGTACAATCTTAAAAAAAA	312
INTRON 4	
EXON 4	
AAAATGAAGAAGTAATCTGAAAACATCCCTGCTGAAATGCTTTATACATTTCCAGGCTGACGCTGACGGCAACGGGTTAA	320
INTRON 4 EXON 5	
EcoRI	
TTGACTACGACGAATTCGTCACCGCAACAGTGCATATGAACAAACTGGATAGAGAAGAGCACCTTTACACAGCATTCCAG	32
	,
EXON 5	•
EcoR I	
TATTTCGACAAGGACAACAGCGGGTAAGTTGAACGTTAAAATGATACAGCTGGTACCTGAATTCTGGACAACACATATCA	33
	i
INTRON 5	-
EXON 5	•
TAACAGGACACATATATATCGTTTATCTCACAGGTACATTACTAAAGAAGAGCTTGAGCACGCCTTGAAGGAGCAAG	- 3
	_
INTRON 5 EXON 6	-
GTTGTATGACGCCGATAAAATCAAAGACATCATCTCCGATGCCGACTCTGACAATGTAAGGAACAAACA	Ţ
GTTGTATGACGCCGATAAAATCAAAGACATCATCTCCGATGCCGACTCTGAG	<u>-</u> 3
	4
EXON 6	-

Fig. 35E

CDPK treue Map (1 > 4165)	Site and Sequence
AGCCGACAAACTAAACTATAGAAAC	Site and Sequence CACATCATGATATCAAATTTTGAGGTGGCGGTGCTACAGAAATAGAACCCAGT
	INTRON 6
ACCAAAATGACTAACTTGTCATGA	TTAGTTGTTCCTCGTAACTGAACATTTGTGTTCTTAGTTTCTTATTGTTAAACC
	INTRON 6
AAGACTTAAATTCACTTTTGCACAT	GCAGGATGGAAGGATAGATTATTCAGAGTTTGTGGCGATGATGAGGAAAGGGAC
INTRON 6-	EXON 7—
	AAGAAGAGGCGAGACATAGTCCTATAGTGAAGTGAAGCAGWAAGTGTGTAATGTA
EXC	DN 7
ATGTGTATAGCAGCTCAAACAAGCA	AATTTGTACATCTGTACACAAATGCAATGGGGTTACTTTTGCAACTTAGTTCATG
GATGGTTGTGTACGTTGTGCTATTG	ATTGCAAGTGATTTGAAAGACATGCATACTTAGGAACTGAGAAAGATAGAT
TACTGCTAGAGACAGAACAATAGGA	TKKYAATTCAGYAAGTGYGTATTTCAGAAGACTACAGCTGGCATCTATTATTCTC
	TGCATTTGAGAGAACAATATGCAACAAGATCGAGCTCCCTATAGTGAGTCGTATT

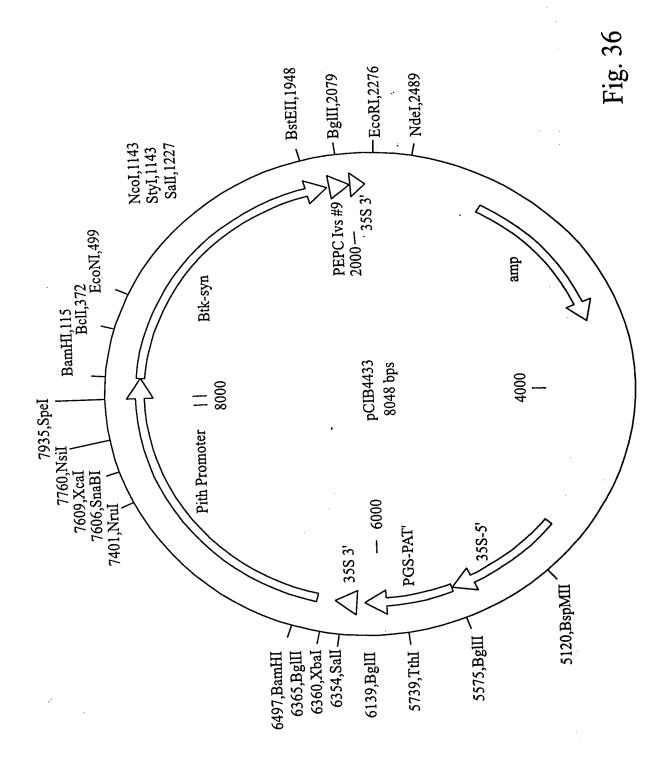


Fig. 37A

1 ATGGACAACA ACCCCAACAT CAACGAGTGC ATCCCCTACA ACTGCCTGAG CAACCCCGAG NetAspAsn AsnProAsn IleAsnGluCys IleProTyr AsnCysLeu SerAsnProGlu
61 GTGGAGGTGC TGGGCGCGA GCGCATCGAG ACCGGCTACA CCCCCATCGA CAICAGCGTG
121 AGCCTGACCC AGTTCCTGCT GAGCGAGTTC GTGCCCGGCG CCGGCTTCG1 GCTGGGCG10
181 GTGGACATCA TCTGGGGCAT CTTCGGCCCC AGCCAGTGGG ACGCCTTCCT GGGGCAGATO
241 GAGCAGCTGA TCAACCAGCG CATCGAGGAG TTCGCCCGCA ACCAGGCCAT CAGCGCCAT CAGCGCAT CAGCGCCAT CAGCACAT CAGCGCCAT CAGCGCAT CAGCGCCAT CAGCGCCAT CAGCGCCAT CAGCGCCAT CAGCGCCAT CAGCGCAT CAGCGCAT CAGCGCAT CAGCGCAT CAGCGCAT CAGCGCAT CAGCGCAT CAGCGCAT CAGCACAT CAGCGCAT CAGCGCAT CAGCGCAT CAGCGCAT CAGCGCAT CAGCGCAT CAGCAT CAGCGCAT CAGCGCAT CAGCGCAT CAGCAT CAGCGCAT CAGCAT
301 GAGGGCCTGA GCAACCTGTA CCAAATCTAC GCCGAGAGCT TCCGCGAGTG GGAGGCCGAGTG ACCAACTGAACCTGAACCTGAACCTACAACCTACAACCTACAACCTACAACCTACAACCTACAACCTACAACCTACAACCTACAACA
361 CCCACCAACC CCGCCCTGCG CGAGGAGATG CGCATCCAGT TCAACGACAT GATGAGAGATA ACCTCAGACAT GATGAGAGATA ACCTCAGACAT GATGAGAGAGATA ACCTCAGACAT ACCTCAGACAT GATGAGAGAGATA ACCTCAGAGAGAGATA ACCTCAGAGAGAGATA ACCTCAGAGAGAGATA ACCTCAGAGAGAGATA ACCTCAGAGAGAGATA ACCTCAGAGAGAGATA ACCTCAGAGAGAGATA ACCTCAGAGAGAGATA ACCTCAGAGAGAGATA ACCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
ProThrAsh PIOAIABEC MIGGERS CAGAACTACC AGGTGCCCCT GCTGAGCGTG 421 CTGACCACCG CCATCCCCCT GTTCGCCGTG CAGAACTACC AGGTGCCCCT GCTGAGCGTG LeuThrThr AlaIlePro LeuPheAlaVal GlnAsnTyr GlnValPro LeuLeuSerVal
LeuThrThr AlailePio Leurichico de Leurichico
TyrValGin AlaAlaAsh Beantologue 541 CGCTGGGGCT TCGACGCCGC CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC 541 CGCTGGGGCT TCGACGCCG CACCATCAAC AGCCGCTACA ACGACCTGAC CCGCCTGATC ArgTrpGly PheAspAla AlaThrileAsh SerArgTyr AshAspLeu ThrArgLeuile ArgTrpGly PheAspAla AlaThrileAsh CACCG GCCTGGAGCG CGTGTGGGGT
ArgTrpGly PheAspAla Alumition 601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCG CGTGTGGGGT 601 GGCAACTACA CCGACCACGC CGTGCGCTGG TACAACACCG GCCTGGAGCT ArgValTrpGly 61 GlyAsnTyr ThrAspHis AlaValArgTrp TyrAsnThr GlyLeuGlu ArgValTrpGly 661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 662 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 663 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 664 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 665 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 666 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 667 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 668 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 669 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 660 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 660 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 661 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 662 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTG 663 CCCGACAGCC GCGACTGGAT CAGGTACAAC CAGTTCCGCC GCGAGCTGAC CCTGACCGTGAC CCTGACCGTGAC CCTGACCGTGAC CCTGACCGTGAC CCTGACCGTGAC CCTGACCGC GCGACCTGAC CCTGACCGTGAC CCTGACCGTGAC CCTGACCGTGAC CCTGACCGC CCTGACCACCAC CCTGACCACCACCACCACCACCACCACCACCACCACCACCACC
ProAspSer AlgASp119 11010 5 2
LeuAspile Valberles -
Serginled initiations of the serginled initiation of the s
Argglyser Aradinos,
901 AACAGCATCA CCATCTACAC CGACGCCCAC CGCGGCGAGT ACTACTGGAG CGGCCACGAGAGAGAGAGAGAGAGAGAGAGAGAGA
IleMetAla SerProVal GlyPheSerGly Floorand ATGGCCAGGG AGTGTACCGC 1021 ATGGCCAACG CTGCACCTCA GCAGCGCATC GTGGCACAGC TGGGCCAGGG AGTGTACCGC MetGlyAsn AlaAlaPro GlnGlnArgIle ValAlaGln LeuGlyGln GlyValTyrArg
MetglyAsh Alamatata MetglyAsh Alamatata 1081 ACCCTGAGCA GCACCCTGTA CCGTCGACCT TTCAACATCG GCATCAACAA CCAGCAGCTG
ThrLeuser Serinization of the Charlet of the Charle
SerValleu AspGlyThr Glurnentary 1201 TACCGCAAGA GCGGCACCGT GGACAGCCTG GACGAGATCC CCCCTCAGAA CAACAACGTG TyrArgLys SerGlyThr ValAspSerLeu AspGluIle ProProGln AsnAsnAsnVal

Fig. 37B

	•	
1261 C	CACCTCGAC AGGGCTTCAG CCACCGTCTG ProProArg GlnGlyPhe SerHisArgLeu	AGCCACGTGA CCATGTTCCG CAGTGGCTTC SerHisVal SerMetPhe ArgSerGlyPhe
1321 A	GCAACAGCA GCGTGAGCAT CATCCGTGCA	CCTATGTTCA GCTGGATTCA CCGCAGTGCG ProMetPhe SerTrpIle HisArgSerAla
1381 9	GAGTTCAACA ACATCATCCC CAGCAGCCAG	ATCACCCAGA TCCCCCTGAC CAAGAGCACG IleThrGln IleProLeu ThrLysSerThr
1441 A	AACCTGGGCA GCGGCACCAG CGTGGTGAAG AsnLeuGly SerGlyThr SerValValLys	GGCCCCGGCT TCACCGGCGG CGACATCCTG GlyProGly PheThrGly GlyAspIleLeu
1501	CGCCGCACCA GCCCCGGCCA GATCAGCACC ArgArgThr SerProGly GlnIleSerThr	CTGCGCGTGA ACATCACCGC CCCCGGGGC LeuArgVal AsnIleThr AlaProLeuSer
1561	CAGCGCTACC GCGTCCGCAT CCGCTACGCC GlnArgTyr ArgValArg IleArgTyrAla	S AGCACCACCA ACCIGCAGII COMMISTARSER A SETTHITH ASHLEUGIN PHEHISTHISET
	lleaspery Argriculo 110110	TTCAGCGCCA CCATGAGCAG CGGCAGCAAC PheSerAla ThrMetSer SerGlySerAsn TTCACCACCC CCTTCAACTT CAGCAACGGC
	CTGCAGAGCG GCAGCTTCCG CACCGTGGGC LeuGlnSer GlySerPhe ArgThrValGly	y PheThrThr ProPheAsh Fheberhands
	AGCAGCGTGT TCACCCTGAG CGCCCACGT SerSerVal PheThrLeu SerAlaHisVa	1 PheAsnSer GlyAshGlu Vallyllions
1801	Argilegia incluir a	C TTCGAGGCCG AGTACGACCT GGAGAGGGCT r PheGluAla GluTyrAsp LeuGluArgAla
1861	GINLYSAIA VAINONGIA	C AGCAACCAGA TCGGCCTGAA GACCGACGTG r SerAsnGln IleGlyLeu LysThrAspVal
1921	Thraspryl hisilensp can	T TTAGTTGAGT GTTTATCTGA TGAATTTTGT n LeuValGlu CysLeuSer AspGluPheCys
1981	CTGGATGAAA AAAAAGAATT GTCCGAGAA	A GTCAAACATG CGAAGCGACT INGTAINTS S ValLysHis AlaLysArg LeuSerAspGlu
2041	CGGAATTTAC TTCAAGATCC AAACTTTAG ArgAsnLeu LeuGlnAsp ProAsnPheAr	GA GGGATCAATA GACAACTAGA CCGTGGCTGG GG GlylleAsn ArgGlnLeu AspArgGlyTrp
2101	AGAGGAAGTA CGGATATTAC CATCCAAGG ArgGlySer ThrAspIle ThrIleGlnGl	GA GGCGATGACG TATTOTAL ANTAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
2161	ACGCTATTGG GTACCTTTGA TGAGTGCTAThrLeuLeu GlyThrPhe AspGluCysT	AT CCAACGTATT TATATCAAMI LYSILeAspGlu yr ProThrTyr LeuTyrGln LysIleAspGlu
2221	TCGAAATTAA AAGCCTATAC CCGTTACC SerLysLeu LysAlaTyr ThrArgTyrG	AA TTAAGAGGGT ATATCGAAGA TAAGAAAAAAAAAAA
2281	TTAGAAATCT ATTTAATTCG CTACAATG LeuGluile TyrLeuile ArgTyrAsnA	CC AAACACGAAA CAGTAAATGI ValProGlyThr la LysHisGlu ThrValAsn ValProGlyThr
2341	GGTTCCTTAT GGCCGCTTTC AGCCCCAA GlySerLeu TrpProLeu SerAlaProS	GT CCAATCGGAA AATGTGGGGAAAG er ProlleGly LysCysGly GluProAsnArg
2401	L TGCGCTCCGC ACCTGGAGTG GAACCCGG CysAlaPro HisLeuGlu TrpAsnProA	AC CTAGACTGCA GCTGCAGGGA AspGlyGluLys sp LeuAspCys SerCysArg AspGlyGluLys
2461	l TGCGCCCATC ATTCCCATCA TTTCTCCT CysAlaHis HisSerHis HisPheSerL	eu AsplieAsp ValGlyCys ThrAspLeuAsn
252	l GAGGACTTAG GTGTATGGGT GATATTCA GluAspLeu GlyValTrp ValIlePheI	AG ATTAAGACGC AAGAIGGCCA ISAlaArgLeu Lys IleLysThr GlnAspGly HisAlaArgLeu
258	1 GGAAATCTAG AATTTCTCGA AGAGAAAC GlyAsnLeu GluPheLeu GluGluLysE	CCA TTAGTAGGAG AAGCACTAGC TCGTGTGAAA Pro LeuValGly GluAlaLeu AlaArgValLys

Fig. 37C

	ArgAlaGlu LysLysTrp ArgAspLysArg	GAAAAATTGG AATGGGAAAC AAATATTGTT GluLysLeu GluTrpGlu ThrAsnIleVal
	TyrLysGlu AlaLysGlu ServalAspAla	TTATTTGTAA ACTCTCAATA TGATAGATTA LeuPheVal AsnSerGln TyrAspArgLeu
	GlnAlaAsp ThrAshile AlaMetilenis	GCGGCAGATA AACGCGTTCA TAGCATTCGA AlaAlaAsp LysArgVal HisSerIleArg
	GluAlaTyr LeurroGiu Leuservaille	CCGGGTGTCA ATGCGGCTAT TTTTGAAGAA ProGlyVal AsnAlaAla IlePheGluGlu
	LeuGluGly Argilerne Thratarneser	CTATATGATG CGAGAAATGT CATTAAAAAT LeuTyrAsp AlaArgAsn VallleLysAsn
	GlyAspPhe AsnAsnGly Leusercyslip	AACGTGAAAG GGCATGTAGA TGTAGAAGAA AsnValLys GlyHisVal AspValGluGlu
	GlnAsnAsn Hisargser vaileuvalval	CCGGAATGGG AAGCAGAAGT GTCACAAGAA ProGluTrp GluAlaGlu ValSerGlnGlu
	ValArgVal CysProGiy ArgGiyiyiii	CTTCGTGTCA CAGCGTACAA GGAGGGATAT LeuArgVal ThrAlaTyr LysGluGlyTyr
	GlyGluGly Cysvaling TientsGrutte	GAGAACAATA CAGACGAACT GAAGTTTAGC GluAsnAsn ThrAspGlu LeuLysPheSer
3181	AACTGTGTAG AAGAGGAAGT ATATCCAAAC AsnCysVal GluGluGlu ValTyrProAsn	AACACGGTAA CGTGTAATGA TTATACTGCG AsnThrVal ThrCysAsn AspTyrThrAla
3241	ACTCAAGAAG AATATGAGGG TACGTACACT ThrGlnGlu GluTyrGlu GlyThrTyrThr	. Delargion in gong - 1 - 1 -
	GAAAGCAATT CTTCTGTACC AGCTGATTATG	Middelina - j
3361	GATGGACGAA GAGACAATCC TTGTGAATCT AspGlyArg ArgAspAsn ProCysGluSe	AACAGAGGAT ATGGGGATTA CACACCACTA AsnArgGly TyrGlyAsp TyrThrProLeu
	CCAGCTGGCT ATGTGACAAA AGAATTAGAQ ProAlaGly TyrValThr LysGluLeuGl	1 Tyllhollo Oldens
3481	mm ca m	C GTGGACAGCG TGGAATTACT TCTTATGGAG e ValAspSer ValGluLeu LeuLeuMetGlu
3541	GAATAA Glu	

